



# STIC Search Report

## Biotech-Chem Library

STIC Database Tracking Number 179593

**TO: Sean McGarry**  
**Art Unit: 1635**  
**Location: REM/2D19/2C18**  
**Serial Number: 09/913858**

**Monday, February 27, 2006**

**From: Beverly Shears**  
**Location: Biotech-Chem Library**  
**REM 1A54**  
**Phone: 571-272-2528**  
**beverly.shears@uspto.gov**

### Search Notes

#### Published Applications Database - November 2005

Published\_Applications Nucleic Acid and Published\_Applications Amino Acid database searches now generate two sets of results each. The Published\_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published\_Applications\_New databases; older published applications make up the Published\_Applications\_Main databases.

Searches run against Nucleic Acid Published\_Applications produce two sets of results, with the extensions **.rnpbm** (Published\_Applications\_NA\_Main) and **.rnpbn** (Published\_Applications\_NA\_New).  
Searches run against Amino Acid Published\_Applications produce two sets of results, with the extensions **.rapbm** (Published\_Applications\_AA\_Main) and **.rapbn** (Published\_Applications\_AA\_New).

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 19, 2006, 15:34:03 ; Search time 10739 Seconds  
(without alignments)  
11634.408 Million cell updates/sec

Title: US-09-913-858C-1  
Perfect score: 2198  
Sequence: 1 actaactcaaacgctgcatt.....aaaaaaaaaaaaaaaaaaaaa 2198

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl.\*  
1: gb\_ba.\*  
2: gb\_in.\*  
3: gb\_env.\*  
4: gb\_om.\*  
5: gb\_ov.\*  
6: gb\_pat.\*  
7: gb\_ph.\*  
8: gb\_pr.\*  
9: gb\_ro.\*  
10: gb\_sts.\*  
11: gb\_sv.\*  
12: gb\_un.\*  
13: gb\_vi.\*  
14: gb\_hcg.\*  
15: gb\_pl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2198	100.0	2198	6	BD270213 Alpha 1,3
2	2198	100.0	2198	6	AX033383 Sequence
3	2191.6	99.7	2198	15	Y18529 Vigna radia
4	1078.6	49.1	2027	15	AY082444 Medicago
5	1068.2	48.6	2134	15	AY082445 Medicago
6	837.2	38.1	1569	15	AJ891040 Populus t
7	690	31.4	1506	15	AJ404860 Arabidops
8	690	31.4	1729	15	AJ345084 Arabidops
9	686.8	31.2	1736	15	AY302219 Arabidops
10	685.2	31.2	1319	15	AY117132 Arabidops
11	678.8	30.9	1542	15	AJ345085 Arabidops
12	678.8	30.9	1607	15	AY184990 Arabidops
13	678.8	30.9	1725	15	BT002570 Arabidops
14	678.8	30.9	1938	15	AY054522 Arabidops
15	664.8	30.2	1568	15	AY184991 Arabidops
16	664.8	30.2	1834	15	AJ404861 Arabidops
17	646	29.4	1633	15	HVU582181 Hordeum v
18	644.6	29.3	1419	15	AJ582955 Oryza sat

19	644.4	29.3	1750	15	TAE582182	AJ582182 Triticum
20	644.2	29.3	2097	15	AK099681	AK099681 Oryza sat
21	534	24.3	658	15	MTR416755	AJ416755 Medicago
22	424.6	19.3	3124	15	AY557602	AY557602 Medicago
23	362.6	16.5	1602	15	PPA429145	AJ429145 Physcomit
24	349	15.9	787	15	AF277228	AF277228 Arabidops
25	346	15.7	588	15	AF277229	AF277229 Arabidops
26	274	12.5	783	15	AY043277	AY043277 Arabidops
27	254.2	11.6	625	15	AF426947	AF426947 Arabidops
28	237.6	10.8	9705	14	AP007454	AP007454 Lotus cor
29	209.4	9.5	2069	6	AX105537	AX105537 Sequence
30	209.4	9.5	2124	6	AX105540	AX105540 Sequence
31	209.4	9.5	2165	6	AX105543	AX105543 Sequence
32	209.4	9.5	2232	6	AX105546	AX105546 Sequence
33	209.4	9.5	2808	6	AX105536	AX105536 Sequence
34	209.4	9.5	2863	6	AX105539	AX105539 Sequence
35	209.4	9.5	2904	6	AX105542	AX105542 Sequence
36	209.4	9.5	2971	6	AX105545	AX105545 Sequence
37	209.4	9.5	3714	6	AX105535	AX105535 Sequence
38	178.8	8.1	104679	15	AC011807	AC011807 Arabidops
39	171	7.8	81875	15	AP000419	AP000419 Arabidops
40	155	7.1	89134	14	AP004162	AP004162 Oryza sat
41	155	7.1	110000	15	AP008214	Continuation (233
42	155	7.1	141319	15	AP004457	AP004457 Oryza sat
43	105	4.8	105	6	BD270214	BD270214 Alpha 1,3
44	105	4.8	105	6	AX033385	AX033385 Sequence
45	90.4	4.1	715	15	AY486752	AY486752 Hevea bra

ALIGNMENTS

RESULT 1  
BD270213  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

BD270213  
Alpha 1,3-fucosyltransferase r36247.  
BD270213  
BD270213.1 GI:33079981  
JP 2002536978-A/1.  
unidentified  
unclassified  
unclassified  
Altman, F.  
Alpha 1,3-fucosyltransferase r36247  
Patent: JP 2002536978-A 1 05-NOV-2002;  
FRIEDRICH ALTMANN  
OS  
JP 2002536978-A/1  
PD 05-NOV-2002  
PD 17-FEB-2000 JP 2000599878  
PR 18-FEB-1999 AT A 270/99  
PI FRIEDRICH ALTMANN  
PC C12N15/09,A01H5/00,A01K67/033,A61K38/45,A61P37/08,  
PC C12N5/10,C12N9/10,C12P19/44,C12Q1/68,C12N15/00,C12N5/  
PC A61P43/00,  
PC 00,C12N5/00,  
PC A61K37/52  
CC Description of Unknown Organism:plant  
FH Key Location/Qualifiers  
FT source  
FT Location/Qualifiers  
1..2198  
/organism="unidentified"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32644"

Query Match 100.0%; Score 2198; DB 6; Length 2198;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;







QY 841 GCACCACTGAGCGCAAAATGAGCTGCTCTTGCAGCTGCTTCAATTTCCAAATGTTGGT 900  
 DB 841 GCACCACTGAGCGCAAAATGAGCTGCTCTTGCAGCTGCTTCAATTTCCAAATGTTGGT 900  
 QY 901 GCTCGAAATTTCCGGTTGCAAGCTCTTGAAGCCCTTCAAAATCAAAATCAAAATGAT 960  
 DB 901 GCTCGAAATTTCCGGTTGCAAGCTCTTGAAGCCCTTCAAAATCAAAATCAAAATGAT 960  
 QY 961 TCTTATGGTGTGTCACAGAAACCGTGATGGAAGAGTGAAACAAAGTGAAGCCCTGAAG 1020  
 DB 961 TCTTATGGTGTGTCACAGAAACCGTGATGGAAGAGTGAAACAAAGTGAAGCCCTGAAG 1020  
 QY 1021 CACTACAAATTTAGCTTAGCGTTGAAATTCGAATCAGGAAGATTATGTAACCTGAAAA 1080  
 DB 1021 CACTACAAATTTAGCTTAGCGTTGAAATTCGAATCAGGAAGATTATGTAACCTGAAAA 1080  
 QY 1081 TTCTTCCAAATCCCTTGTGCTGGAACCTGCTCCTGCTGTTGTTGCTGCTCCAAATATTTCAG 1140  
 DB 1081 TTCTTCCAAATCCCTTGTGCTGGAACCTGCTCCTGCTGTTGTTGCTGCTCCAAATATTTCAG 1140  
 QY 1141 GACTTTGCTCTCTCTGTTCAATTTTACATATTAAAGAGATAGAGGATGTTGAGTCT 1200  
 DB 1141 GACTTTGCTCTCTCTGTTCAATTTTACATATTAAAGAGATAGAGGATGTTGAGTCT 1200  
 QY 1201 GTTCCAAGACCATGAGATCTAGCAGAAATCCCGAAGCATATAATCAATCAATTCAGG 1260  
 DB 1201 GTTCCAAGACCATGAGATCTAGCAGAAATCCCGAAGCATATAATCAATCAATTCAGG 1260  
 QY 1261 TGGAGTATGAGGTCATCTGACTCTCTTCAAGCCCTTGTGGATATGGCAGCTGTGCAT 1320  
 DB 1261 TGGAGTATGAGGTCATCTGACTCTCTTCAAGCCCTTGTGGATATGGCAGCTGTGCAT 1320  
 QY 1321 TCATCGTCCCTCTTTGCAATTCATCTGSCCACTGAGTATAGAGAGGAGAAATAAT 1380  
 DB 1321 TCATCGTCCCTCTTTGCAATTCATCTGSCCACTGAGTATAGAGAGGAGAAATAAT 1380  
 QY 1381 CCAAGCCTTAAGACAGCTCTTGAAGTGCATGAGGCGGAGGAGGAGGAGGAGGAGGAGG 1440  
 DB 1381 CCAAGCCTTAAGACAGCTCTTGAAGTGCATGAGGCGGAGGAGGAGGAGGAGGAGGAGG 1440  
 QY 1441 TATGTGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1500  
 DB 1441 TATGTGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1500  
 QY 1501 ACTCTGAATGCTGTAAGGCTGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1560  
 DB 1501 ACTCTGAATGCTGTAAGGCTGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1560  
 QY 1561 GTATGGAAGACTGAAAGCCCTGAAAGTTTAAAGAGGGGGAGTGTCTTAAAGCTCTACAAA 1620  
 DB 1561 GTATGGAAGACTGAAAGCCCTGAAAGTTTAAAGAGGGGGAGTGTCTTAAAGCTCTACAAA 1620  
 QY 1621 ATATACCAATTTGGCTTGACACAGAGAGAGCTCTTTATACCTTCAGCTTCAAAAGGTGAT 1680  
 DB 1621 ATATACCAATTTGGCTTGACACAGAGAGAGCTCTTTATACCTTCAGCTTCAAAAGGTGAT 1680  
 QY 1681 GCTGATTTTCAAGAGTCACTTGAGAACCAATCTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1740  
 DB 1681 GCTGATTTTCAAGAGTCACTTGAGAACCAATCTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1740  
 QY 1741 TAGCATGCGCTAAATGTTAGCTCTCTCTACCTGAATTTAGCTTCACTTACCTGAGCACTA 1800  
 DB 1741 TAGCATGCGCTAAATGTTAGCTCTCTCTACCTGAATTTAGCTTCACTTACCTGAGCACTA 1800  
 QY 1801 GCTAGATTTTGAAGATGAGTATGCGATGAGTATGCGATGAGTATGCGATGAGTATGCGATGAG 1860  
 DB 1801 GCTAGATTTTGAAGATGAGTATGCGATGAGTATGCGATGAGTATGCGATGAGTATGCGATGAG 1860  
 QY 1861 TCTTGGCCAACTCATTTGATGTTTGTATAGACATCACATTTAAATTTTAACTTTGTTTC 1920  
 DB 1861 TCTTGGCCAACTCATTTGATGTTTGTATAGACATCACATTTAAATTTTAACTTTGTTTC 1920

QY 1921 TGTAGAAGTGCAATCCATATTTAATGCTTTAGTGTCTTTATCTGATCATCTAGA 1980  
 DB 1921 TGTAGAAGTGCAATCCATATTTAATGCTTTAGTGTCTTTATCTGATCATCTAGA 1980  
 QY 1981 AGTCACAGTTCTTGTATATGTCAGTGAAACTGAAATCTAATAGAGGATCAGATGTTT 2040  
 DB 1981 AGTCACAGTTCTTGTATATGTCAGTGAAACTGAAATCTAATAGAGGATCAGATGTTT 2040  
 QY 2041 CACTCAAGACACATTTACTTCTATGTTGTTTGTGATGATCTCGAGCTTTTGTAGTGTCTG 2100  
 DB 2041 CACTCAAGACACATTTACTTCTATGTTGTTTGTGATGATCTCGAGCTTTTGTAGTGTCTG 2100  
 QY 2101 GAACGTGCTGCTGTTGAGCACCTGTTATGCTTCAGTGTACTGTCAGTGTGTTATC 2160  
 DB 2101 GAACGTGCTGCTGTTGAGCACCTGTTATGCTTCAGTGTACTGTCAGTGTGTTATC 2160  
 QY 2161 GTTTTGTGACCTCTAAAAAATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 2198  
 DB 2161 GTTTTGTGACCTCTAAAAAATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 2198

RESULT 4  
 AY082444 2027 bp mRNA linear PLN 02-MAR-2005  
 LOCUS Medicago sativa clone MSI-3Fta alpha 1,3 fucosyltransferase mRNA,  
 DEFINITION complete cds.  
 ACCESSION AY082444  
 VERSION AY082444.1 GI:37543455  
 KEYWORDS Medicago sativa  
 SOURCE Medicago sativa  
 ORGANISM Medicago sativa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;  
 Medicago.  
 REFERENCE 1 (bases 1 to 2027)  
 AUTHORS Sourrouille,C., Kiefer-Meyer,M.-C., Faye,L. and Gomord,V.  
 TITLE Direct Submission  
 JOURNAL Submitted (06-MAR-2002) LTI-CNRS UMR6037, Universite de Rouen, Bat.  
 Extension Biologie, Mont Saint Aignan 76821, France  
 FEATURES  
 location/Qualifiers  
 1..2027  
 /organism="Medicago sativa"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:3879"  
 /clone="MSI-3Fta"  
 202..1722  
 /codon\_start=1  
 /product="alpha 1,3 fucosyltransferase"  
 /protein\_id="AA199370.1"  
 /db\_xref="GI:37543456"  
 /translation="MGLVSRITTTTTOGLPVSVSTTTPKKNLMLPLFVALVLI  
 AEAFLGRLDMAKNAMVADLFYRSRAVVGDDDFGLTGVGDKNLELERETCEWLER  
 EDATVYSRNFKNEPFGVSGAEQWKSVCVKGDFNGDRKPEAFGLPQQAGTASVLR  
 SMESAQTYAENNLAMARRGYHIVMTTSLSDVPVGYFSAEYDIMAPIKPTBKALA  
 AAPTISNCGANFRLQALEKTNISIDSYGSHNRDGRVDKLETITRYKFSAPEN  
 SNEDVYTEKFSVLVAGTTPVVVGPNIODPAPSPDFLYIKLELDEVESVAKSMRYL  
 AENPEANHSLRWKYGCPDSKALVDMAAVHSSCLICHLATKSREKEKSPDFKKR  
 PKCTRGSEYTHIYVRGTFFEMESIYLRSSNLTLSSEKTAFLTKTSLNHPVWKP  
 ERPEILKGGDKLVKVIIPAGLTORQALYTFQFNGDVFDFRSHLESNCPCKEYFV"

Query Match 49.1%; Score 1078.6; DB 15; Length 2027;  
 Best Local Similarity 77.2%; Pred. No. 1.7e-252;  
 Matches 1405; Conservative 0; Mismatches 374; Indels 42; Gaps 6;

QY 184 GGAATTTGCGAGTTGGGGCGCAATTTGAATGATGGTCTGTTGACGAATCTTTGAGGCTCG 243  
 DB 172 GGAATTTGAGATTGGAGGTAGATTAAATTGATGGTCTGCTTTCAAGAAACAACAACA 231  
 QY 244 AGAAGAGATGTTGCCCAACAAGACAGCTTACCGCTTTTGGCTCCGGGAGGCAACCAAG 303  
 DB 232 ACAACCAAGAGGTTTACCAG-----TTTCAGTTTTCAGTTTCAACAACGTTCCGAG 285



QY	304	AGGAAATGAGCAATCTAATGCCTCTTGTGTTGGCCCTTGTGTCATCGCGAGATCGCG	363
Db	286	AGAAATGGTCGAATTTAATGCCCTTTATTGTAGCACCTTGTGGTTATTGGGAGATCGCG	345
QY	364	TTTCTGGGTAGGTGGATATGGCAAAACCGCCCATGGTTGACTCCCTCGCTGACTTTC	423
Db	346	TTTTTGGGTAGGTGGATATGGCTAAGAACGCGAGCTATGGTT-----GCTGACTTG	396
QY	424	TTCTACCGCTCTCGAGCGGTGGTTGAAGGTGACGATTTGGGGTTGGGTTGGTGGCTTCT	483
Db	397	TTCTACCGGTCACTCGGTGGTGTGAAGGTGATGATTTTGGGTTAGAGACAGTTGGTGGT	456
QY	484	GATCGGAATCTGAATCGTATAG-----TTGTGAGGAATGTTGGAGAGGAGGATGCT	537
Db	457	GATAAGAAATTGGAATTTAGAGAGAGAACTTGTGAGGAGTGGTTGGAGAGAGGATGCT	516
QY	538	GTCACTGATTCGAGGGGCTTTTCCAAAGAGCCCTATTATTTTGTCTGGAGCTGATCAGGAG	597
Db	517	GTATACATATTCAGGAACTTTAATAAGGAACCTGTTTTTGTCTGGAGCTGNAACAGGA	576
QY	598	TGGAATCGGTTCGGTTGGATGATAAATTTGGGTTTGTGGGGATAGAAAGCCAGATGCC	657
Db	577	TGGAAGTCATGTTCACTGGGATGATAAATTTGGGTTTAAATGGGGACCGGAAACCTGAGGCT	636
QY	658	GCATTTGGGTTACCTCAACCAAGTGAACAGCTAGCATTTCTGCGATCAATGGNATCAGCA	717
Db	637	GCATTTGGGTTACCTCAGCAAGCTGGAACAGCAAGTGTCTGAGATCAATGGAGTCGGCA	696
QY	718	GAATATCTATGCTGAGAACCAATATTCGCATGGCAAGACGAGGGGATATAACATCGTAATG	777
Db	697	CAATCATATGCAGAACCAATCTTGCCATGGCACGACGAGGGGATATCACATTTGTAATG	756
QY	778	ACAACCACTATCTTCGGATGTTCTGTGTGGATATTTTTCATGGGCTGAGTATGATATG	837
Db	757	ACAACCACTATCTGACGTCCTGTGTGGATATTTTTCATGGGCTGAGTATGATGATC	816
QY	838	ATGGCACAGTCAGCGCGGAACCTGAGCTGCTTTCGAGCTGCTTTTCCAAATTCG	897
Db	817	ATGGCACGGAATAAGCGAATAAATCTGAAAAGCTCTTCGAGCTGCTTTTTCAAATTCG	876
QY	898	GGTGTCTCGAAATTTCCGGTTGCAAGCTCTTTGAGCGCCCTTGAAAAATCAACATCAAAAT	957
Db	877	GGTGTCTCGAAATTTCCGATTGCAAGCTCTCGAAGCCCTAGAAAAACAAACATCTCGATC	936
QY	958	GATTCCTATGTTGGTTGTACAGGAACCGGTGATGGAAGAGTGAAACAAAGTGAAGCCCTG	1017
Db	937	GACTCTTATGTTAGTTGTATAGGAATCGTGATGGAAGAGTGGACAAACTGGAAACCCCTG	996
QY	1018	AAGCACTACAAATTTAGCTTAGCTTTGAAATTCGAATCGAAGAGATTATGTAAGTGA	1077
Db	997	ACGCGCTACAAATTTAGCTTAGCATTTGAAATTCCTAAGAGAGGAGATTATGTAAGTGA	1056
QY	1078	AAATTCCTCAATCCCTTGTGCTGGAACCTGCTCCCTGCTGGTGTGGTGTCCCAATATTT	1137
Db	1057	AGTTTTTCCAGTCGCTTGTGTGGAACCTATCCCTGCTGGTGTGGTGTCCCAATATTT	1116
QY	1138	CAGGACTTTGCTCCTTCTCTCGTTCAATTTTATATATAATTAAGAGATAGAGGATTTGAG	1197
Db	1117	CAAGATTTTGTCTCTCTGATTCATTTTATATATAATCAAGAACTAGAGGATTTGAG	1176
QY	1198	TCTGTTGCAAGCAATGAGATATCTAGCAGAAATCCCGAAGCATATATCAATCATTTG	1257
Db	1177	TCTGTTGCAAGTCCATGAGATACCTAGCAGAAACCCCTGAGCATATATCATTCATTTG	1236
QY	1258	AGGTGGAAGTATGAGGTCATCTGACTCCTTCAAGCGCCCTTGTGGATATGGCAGCTGTG	1317
Db	1237	AGGTGGAAGTATGGAAGGCCATCTGATTTCTTCAAGCCCTTGTGGATATGGCAGCTGTG	1296
QY	1318	CATTTCATCGTGGCTCTTTGCAATTCATCTTGGCCACAGTGTGAGTAGAGAGGAGAAAT	1377
Db	1297	CATTTCATCTTGGCGCTTTGCAATTCATCTTGGCCACAAAGAGTAGAGAGGAGAGAAG	1356
QY	1378	AATCAAGCTTTAAGAGAGCGTCTTTGCAAGTGCCTAGAGGGCCAGAAACCGGTATATCAT	1437
Db	1357	AGCCCAAGACTTCAAGAGCGGACCTTGCAGTGCATCGAGGGTCAGAACTGTATATCAT	1416
QY	1438	ATCTATGTCAGAGAAAGGGGAAGTTTGAGATGGAGTCCATTTACTGAGGTCTAGCAAT	1497
Db	1417	ATCTATGTCAGAGAAAGGGGAACATTTGAGATGGAGTCCATTTACTTGAGATCTAGCAAT	1476
QY	1498	TTAACTCTCAATCTGTGTAAGGCTGCTGTTGTTTGAAGTTCACATCCCTGATCTTGTG	1557
Db	1477	TTAACTCTCTGAGTCTCTCAAGACTGCTGTTCTTAGAAGTTCACGTCCTGATCATGTT	1536
QY	1558	CCTGTATGGAAGACTGAAAGGCTCAAGTTATAAGAGGGGAGTGTCTTTAAACACTCTAC	1617
Db	1537	CCTGTATGGAAGCTTGAAGACCTGAAATTTTAAAGGTGGCGATAAATTTGAAGGTTTAC	1596
QY	1618	AAAAATATACCCAAATTTGGCTTGACACAGAGACAAGCTCTTTATACCTTCAGCTTCAAAGT	1677
Db	1597	AAAAATATACCTCGGGCTTGACACAGAGGCAAGCTCTTTATACCTTCCAGTTCAACGGG	1656
QY	1678	GATGCTGATTTGAGAGTCACTTGGAGAACATCTTGTGCGCAAGTTTGAAGTCATTTT	1737
Db	1657	GATGTTGATTTTGAAGTCACTTGGAAAGCAATCTTGTGCGCAAGTTTGAAGTAAATTTT	1716
QY	1738	GTGTAGCATGCGCTAA-----ATGGTACCTCTGCTTACCTGAATTAGCTTCACTTAG	1790
Db	1717	GTGTAGCATATGTTGAGCTACCGACAATTTACATGAAACACCTAGCATTAGCTCTTTCAC	1776
QY	1791	CTGAGCACTAGCTAGAGTTTATAGGAATGAGTATGGCAGTGAATATGGCAATGCTTTTAT	1850
Db	1777	TAACTGAGAGATGAAGTTTATAGGAATGAGTATGACCATGGAGTCGGCATTTGTTAA	1836
QY	1851	ATGCCCTAGTTTC-TTGGCCCACTCATTTGATGTTT-----TGATTAAGACATC	1896
Db	1837	TGCCCTACCTTACTTTTGGCCCACTCATCGGGGATTTTACATTCAGAAAATATACATGACT	1896
QY	1897	ACACTTTAAATTTTAAACTTGTTCGTAGAAGTGCAATCCCATATTTAATGCTTAGCTTT	1956
Db	1897	AACCATCTTAAACCCCTTTTGTAAAGATACTGAATGTTTCATATTTAATGTTGGTTAT	1956
QY	1957	AGTGTCTTTATCTGATCATCT 1977	
Db	1957	AGTGTTTTACTTGTATTAT 1977	
RESULT 5			
AY082445			
LOCUS			
DEFINITION	Medicago sativa clone MS1-3Ftb alpha 1,3 fucosyltransferase mRNA,	2134 bp	linear
ACCESSION	AY082445		
VERSION	AY082445.1	GI:37543463	
KEYWORDS			
SOURCE	Medicago sativa		
ORGANISM	Medicago sativa		
REFERENCE			
AUTHORS	Sourrouille,C., Kiefer-Meyer,M.-C., Faye,L. and Gomord,V.		
TITLE	Direct Submision		
JOURNAL	Submitted (06-MAR-2002) LTI-CNRS UMR6037, Universite de Rouen, Bat.		
EXTENSION	Biologie, Mont Saint Aignan 76821, France		
FEATURES			
source			
1..2134			
/organism="Medicago sativa"			
/mol_type="mRNA"			
/db_xref="taxon:3879"			
/clone="MS1-3Ftb"			
205..1722			
/codon_start=1			
/product="alpha 1,3 fucosyltransferase"			
CDS			







Db	1486	TCCTACAAATTCACACATGATGATGATTTCAAGAAATCACTTGGGAAGTCAACCCATGTGCA	1545
Qy	1720	AAGTTTGAAGTCATTTTGTGTAG	1743
Db	1546	AAGTTTGAAGTCATTTTGTGTAG	1569
RESULT 7			
ATH404860			
LOCUS			
DEFINITION	Arabidopsis thaliana mRNA for alpha1,3-fucosyltransferase (FucTA gene).		
ACCESSION	AJ404860		
VERSION	AJ404860.1	GI:13992482	
KEYWORDS	alpha 1,3-fucosyltransferase; FucTA gene.		
SOURCE	Arabidopsis thaliana (Chale cress)		
ORGANISM	Arabidopsis thaliana		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.		
AUTHORS	Wilson, I.B., Rendic, D., Freilinger, A., Domic, J., Altmann, F., Mucha, J., Muller, S. and Hauser, M.T.		
TITLE	Cloning and expression of cDNAs encoding alpha1,3-fucosyltransferase homologues from Arabidopsis thaliana		
JOURNAL	Biochim. Biophys. Acta 1527 (1-2), 88-96 (2001)		
PUBMED	11420147		
REFERENCE	2 (bases 1 to 1506)		
AUTHORS	Wilson, I.B.H.		
TITLE	Direct Submission		
JOURNAL	Submitted (11-JUL-2000) Wilson I.B.H., Institut fuer Chemie, Universitaet fuer Bodenkultur, Muthgasse 18, Wien 1190, Austria		
FEATURES	Location/Qualifiers		
source	1..1506		
gene	/organism="Arabidopsis thaliana"		
CDS	/mol_type="mRNA"		
	/db_xref="taxon:3702"		
	/ecotype="Columbia"		
	1..1506		
	/gene="FucTA"		
	1..1506		
	/gene="FucTA"		
	/function="glycosyltransferase; fucose transfer"		
	/codon_start=1		
	/product="alpha1,3-fucosyltransferase"		
	/protein_id="CAC38048.1"		
	/db_xref="GI:13992483"		
	/db_xref="GOA:O9LJK1"		
	/db_xref="UniProt/Swiss-Prot:O9LJK1"		
	/translation="MGVFSNLRGPKIGLTHEELPVANGSTSSSSPSSPKKVVSTEL PICVALVVIIEIGLCRLDNASLVDTLHFTFKSSDLDKVGSGIEKCEWLERVDSVT YSRDFTKDPIFISGNKDFKSCVDVNGVFTSDRKKDDAFLGSHQPGTSLIRSMESA QYQBNLLAQRKGYDVMVTSLSDDVPVGFVSWAEDYINAPVQPKTEKALAAAFIS NCAENFLQALEALMTNKVIDSYGCHNRNDGSEKVEALKHVFKSLAPENTNEED VYTEKPFQSLVAGSVVVGAPNIEFAPSDDSLHIKQMDVDKVAKKMKVYLADND AYNQTLRWKHPGSDSFKALIDMAVHSSCRICIFVATRIREQSEKSEPFKRPCKCT RGSETVVLYHREGRFDMSEIFLDKGNLTLEALESVALKFMSLRYEPIPWKKRPPAS LRGDKLRVHGVIYPIGLTQROALYNFKPEGNSLSLTHIQRPCKPFVVFV"		
ORIGIN			
Query Match	31.4%;	Score 690;	DB 15; Length 1506;
Best Local Similarity	72.0%;	Pred. No. 1.8e-157;	
Matches 900;	Conservative 0;	Mismatches 350;	Indels 0; Gaps 0;
Qy	493	TCGTGAATCGTAGTTGTGAGGAATGGTTGGAGAGGAGGAGTGTGTCACTGATTTTCGAGG	552
Db	256	TCAGGAATAGAAATGCCAGAGTGGTTAGAGAGAGTGATTCAGTTACTTATCTAGA	315
Qy	553	GGCTTTTCCAAAGAGCTATTTTGTGTTCTCGAGCTGATCAGGAGTGGAAAGTCGTGTCG	612
Db	316	GATTTTCACTAAAGATCCGATTTTATCTCTGTGTAGTAAACAAGGACTTCAAAATCGTGCTC	375
Qy	613	GTGGAGTAAATTTGGGTTTGTAGTGGGGATAGAAAGCCAGATGCCCATTTGGGTACCT	672

Db	376	GTGTAATGTGTAATGGGAATTCACCTTCAGATAAGAAACCTGATCGGCTTTTGGATTAAGT	435
Qy	673	CAACCAAGTGGACAGCTAGCATTCTCGCATCAATGAATCAGCAGAAATCTATGCTGAG	732
Db	436	CATCAACCTGGAACCTCAGTATAATCCGTTTCATGGAATCAGCAAGTATTACCAAGAG	495
Qy	733	AACAATATTGCCATGGCAAGACGAGGGGATATAACATCGTAATGACAAACAGCTATCT	792
Db	496	AATAATCTTGCTCAAGCAGCAGCGAAAGTTATGATATTGTGATGACAACTAGTCTGTCA	555
Qy	793	TCGATGTTCTGTTGGATATTTTTCATGGCTGAGTATCATATGATGAGCCAGCTGAG	852
Db	556	TCAGATCTTCTGTTGGGTATTTTTCATGGCGGGAATATGATATTATGGCTCCAGTGCAA	615
Qy	853	CCGAAACTGAAGCTGCTCTTGACAGCTCTTTCATTTTCAATTTGCTGCTCGAAATTTTC	912
Db	616	CCAAAAACAGAGAAAGCTCTTGCTGCTCTTTTATTTTCAATTTGCGCGCTCGGAATTT	675
Qy	913	CGGTTGCAAGCTCTTGAGGCGCTTTGAAAAATCAAAACATCAAAATTTGATTTTATGGTGT	972
Db	676	CGCTGCAAGCTCTTGAAGCTTAAATGAAGACGAATGTTAAGATTGATTTCTTATGGTGT	735
Qy	973	TGTCACAGAACCGTGTATGGAAGAGTGAAACAAAGTGAAGCCCTGAAGCAGCTACAAATTT	1032
Db	736	TGTCACCGAATCGGATGGAGTGTGGAGAGGTTGAAGCTCTTAAGCAGCTACAAATTT	795
Qy	1033	AGCTTAGGTTGAAATTCGAATGAGGAAGATTTATGTAAGTGAATTTCTTCAATATCC	1092
Db	796	AGTCTAGCTTTTGAGAAACACCAACGAGGAGGATTTATGTCAGAGAGATTTCTTCAATCT	855
Qy	1093	CTTCTGCTGGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1152
Db	856	CTAGTCTGAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	915
Qy	1153	TCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1212
Db	916	TCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	975
Qy	1213	ATGAGATATCTAGCAGAAATCCCGAGCATATATCAATCATTTGAGTGAAGTGAAGTATGAG	1272
Db	976	ATGAAGTATCTGCGGATTAACCTGAGCGCTTATATCAGCGCTGAAGTGAAGTGAAGTGAAG	1035
Qy	1273	GGTCCATCTGACTCCTTCAAGGCGCTTGTGATATGGCAGCTGTGCTGCTGCTGCTGCTGCT	1332
Db	1036	GCCCTTTCAGATCTTTTGAAGCAGCTTATGATATGCTGCTGCTGCTGCTGCTGCTGCTGCT	1095
Qy	1333	CTTTGCAATTCATTTGGCCACAGTGAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	1392
Db	1096	CTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1155
Qy	1393	AGAGCTGCTGCAAGTGCAGCTAGAGGCGCAGAAACCGTATATATCTATCTATGTCAGAGAA	1452
Db	1156	AGAGCGCTGCAAAATGACAGAGGCTCAGAGAGGCTTATCAATTTGATGTTAGAGAA	1215
Qy	1453	AGGCGAGGTTTGAAGTGGAGTCCATTTTACCTGAGGCTAGCAATTTTAACTCTGAATGCT	1512
Db	1216	AGAGACGTTTGAATGGAATCCATCTTCTTGAAGGATGGAATCTGACTCTGGAAGCT	1275
Qy	1513	GTGAAGGCTGCTGTTGTTTGAAGTTCATCCCTCGAATCTTGTGCTGCTGCTGCTGCTGCTG	1572
Db	1276	CTGGATCTCGGGTCTTTCGGAAGTTCATGCTCTGAGATATGAACCAATATGAAGAAG	1335
Qy	1573	GAAGGCTGGAAGTTATGAAGGGGGAGTCTTTTAAACTCTACAAATATACCAATTT	1632
Db	1336	GAAGAGCCCGGAGCTTAAAGAGGAGACGGCAAGCTTAGAGTACATGGGATATATCTAT	1395
Qy	1633	GGCTTGACACAGAGACAGCTTTTATACCTTTCAGCTTCAAGGTTGCTGCTGCTGCTGCTG	1692
Db	1396	GGTCTGACTCAAGACAGAGCTCTTTTAACTTCAATTTCAAGTGAAGGAAATTCAGTCTCAG	1455
Qy	1693	AGTCACTTTGGAGAAACAAATCTTGTGCGCAAGTTTGAAGTCAATTTTGTGTA	1742

Db	1456	ACTCACATACAGAGAAACCTTGTCCTCCAAATTCGAAGTTGCTTTGTCTTA	1505	Db	468	GTGATTGTGTAAATGGGATTCACATTCAGATAAGAAACCTGATGGCGCTTTTGGATAAAGT	527
RESULT 8	ATH345084	1729 bp	mRNA	linear	PLN 03-OCT-2002		
LOCUS	Arabidopsis thaliana mRNA for core-alpha1,3-fucosyltransferase 1 (fucT1 gene).						
DEFINITION	ATH345084						
ACCESSION	AJ345084						
VERSION	GI:15722479						
KEYWORDS	core-alpha1,3-fucosyltransferase 1; fucT1 gene.						
SOURCE	Arabidopsis thaliana (thale cress)						
ORGANISM	Arabidopsis thaliana						
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Rosids; eutrosids II; Brassicales; Brassicaceae; Arabidopsis.						
AUTHORS	Bakker, H., Schijlen, E., de Vries, T., Schiphorst, W.E., Jordi, W., Lommen, A., Bosch, D. and van Die, I.						
TITLE	Plant members of the alpha1-->3/4-fucosyltransferase gene family encode an alpha1-->4-fucosyltransferase, potentially involved in Lewis(a) biosynthesis, and two core alpha1-->3-fucosyltransferases						
JOURNAL	PEBS Lett. 507 (3), 307-312 (2001)						
PUBLISHED	1169361						
REFERENCE	2 (bases 1 to 1729)						
AUTHORS	Bakker, H.						
TITLE	Direct Submission						
JOURNAL	Submitted (14-SEP-2001) Bakker H., Plant Research International, Wageningen University and Research centr, droevendaalsesteeg 1, Netherlands 6708PB, NETHERLANDS						
FEATURES	Location/Qualifiers						
source	1..1729						
	/organism="Arabidopsis thaliana"						
	/mol_type="mRNA"						
	/db_xref="taxon:3702"						
	/ecotype="Columbia"						
	/tissue_lib="selique"						
gene	1..1729						
CDS	/gene="fucT1"						
	93..1598						
	/gene="fucT1"						
	/function="glycosyltransferase involved in N-glycan biosynthesis"						
	/codon_start=1						
	/product="core-alpha1,3-fucosyltransferase 1"						
	/protein_id="CAC78979.1"						
	/db_xref="GI:15722480"						
	/db_xref="GOA:Q9LJK1"						
	/db_xref="UniProt/Swiss-Prot:Q9LJK1"						
	/translations="MGVFNLRGPKIGLTHELPVNVANGSTSSSPSPFKRKVSTFL PICVALVITIEIGLCRLDNASIVDLTHFTKSSDLKVGSGIERKQEWLERVDSVT YSRDFTKDPFIIGSNKDPKSCVDCVMGFTSDKPDPAAPGLSHQPGTLSIIRSMESA QYQENNLQALARKGVDIUMTTSLSNDVPVGVSWAEYDIDMAPVQPKTEKALAAAFIS NCAARPLRQALRMKNTVKIDSYGGCHNRDGSVEKVEALHYKFLAFENTNEED YVTEKFPQSLVAGSPVVPVGNPIEFAPSPDFLHKQDDVDKAVAKGKYLADNPD AYNQRLRWKHSDFKALIDMAVHSSCLRCIFVATRIREQEESKSPFKRPCKCT RGSETVYVHLVYRGRPFMESIFLKDGNLTLEASAVLAKFMSLRYEPIWKKERPAS LRGDGLRVHGIVPIGLTRQALYNFKFEGNSLSLTHIQRNPCPKPEVWFV"						
ORIGIN							
Query Match	31.4%;	Score 690;	DB 15;	Length 1729;			
Best Local Similarity	72.0%;	Pred. No. 1.8e-157;					
Matches	900;	Conservative	0;	Mismatches 350;	Indels	0;	Gaps
Qy	493	TCTGAATCGTATAGTTGTGGAGTGGTTCGAGAGGAGGATCGTCAGTATTCGAGG	552	Qy	1573	GAAGGCGCTGAAGTTATAAGAGGGGGAGTGTCTTTAAACTCTACAAAATATACCCAAATT	1632
Db	348	TCAGGAATAGAGAAATCCAGAGTGGTGTAGAGAGTGGATTCACTTACTTATTCAGA	407	Db	1428	GAAGACCCGCGAGCTTAAGAGGAGACGCGCAAGCTTAGAGTACATGGGATATATCCTATT	1487
Qy	553	GGCTTTTCCAAAGACCTATTTTGTCTGGAGCTGATCAGGAGTGGAAAGTCGTGTTCG	612	Qy	1633	GGCTTGACACAGAGACCAAGCTCTTTATACCTTCAGCTTCAAGGTGATGCTGATTCAGG	1692
Db	408	GATTTCACTAAGATCCGATTTTATCTCTGGTAGTAAACAGGACTTCAAAATCGTCTCT	467	Db	1488	GSTCTGACTCAAGAGCAAGCTCTTTACAACTTCAAAATTCGAAGGAATTCAGTCTCAGT	1547
Qy	613	GTTGGATGTAAATTTGGGTTTAGTGGGGATAGAAAGCCAGATCCGCAATTTGGTTACCT	672	Qy	1693	AGTCACCTTGAGAAACAATCCTTGTGCAAGTTTGAAGTCAATTTTGTGTGA	1742

Db	1548	ACTCATACAGAGAAACCCTTGTCGCCAAATTCGAAAGTTGTCTTTGTGCTA	1597
RESULT 9			
AY302219			
LOCUS	AY302219	1736 bp mRNA linear PLN 13-MAY-2005	
DEFINITION	Arabidopsis thaliana alpha 1,3 fucosyltransferase mRNA, complete cds.		
ACCESSION	AY302219	GI:34923183	
KEYWORDS	Arabidopsis thaliana (thale cress)		
SOURCE	Arabidopsis thaliana		
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.		
REFERENCE	Kiefer-Meyer,W.-C., Faye,L. and Gomord,V. Direct Submission Submitted (16-MAY-2003) CNRS UMR 6037, Universite de Rouen, Bat. Extension Biologie-Faculte des Sciences, Mont Saint Aignan 76821, France		
FEATURES	Location/Qualifiers		
source	1..1736		
	/organism="Arabidopsis thaliana"		
	/mol_type="mRNA"		
	/db_xref="taxon:3702"		
CDS	18...1523		
	/codon_start=1		
	/product="alpha 1,3 fucosyltransferase"		
	/protein_id="AAQ83526.1"		
	/db_xref="GI:34923184"		
	/translation="MGVPSNLRGPKIGLTHELPWANGSTSSSPSKRVSTFL PICVALVIIIEGFLICRLDNASLDVLTTHFTKSSDLKVSGIERCOEWLERVDVST YSRDFTKDPIFISGNKDFKSCVDCVMGFTSDKPDAEGLSHQPTLSIIIRMSBA QYQENNLQAARKGYDIWMTSLSSGVPEYFSAEYDINAPVPKTERALAAAFIS NCAARNFLQALEALMKTNIKDISYGCHNRNDGSVEKEALKHYKFSLAPENTNEED AVTEKRFOSLVGPNVVGAPNIIEFPAPSDFSFLHIKQMDVKVAKKMKYLADNP YNOTLRWKHGEPDSFKALIDMAVHSSRLCI FVATRIREQBEKSPFKRPRCKRT RSEVTYHLIYVERGRPFMESIFLKDGNLTLEALESVLAKFMSLRVEPITWKKERPAS LRGDGKLVRHGIPIGLTORQALYNFKPEGNSSLTHIQRNPCPKFEVFV"		
ORIGIN			
Query Match	31.2%;	Score 686.8;	DB 15; Length 1736;
Best Local Similarity	71.8%;	Pred. No. 1.1e-156;	
Matches 898;	Conservative	0;	Mismatches 352; Indels 0; Gaps 0;
Qy	493	TCTGAATCGTATAGTTGTGAGGAATGGTTGGAGAGGGAGGATGCTGCACGTATTCGAGG	552
Db	273	TCCGGAATAGAGATGCCAGGAGTGGTTAGAGAGAGTGGATTCAAGTTACTTATTCTAGA	332
Qy	553	GGCTTTTCCAAGAGCCTATTTTTTCTCGAGCTGATCAGGAGTGAAGTCGTGTCG	612
Db	333	GATTTCACTAAAGATCCGATTTTTTATCTCTGTAGTAACAAGGACTTCAMATCGTCTCT	392
Qy	613	GTTCGATGTAAATTTTGGTTTAGTGGGATAGAAACCCAGATGCCGCAATTTGGGTACCT	672
Db	393	GTTCGATGTGTAATGGATTCACCTCAGATAAGAAACCTGATCCGCTTTTGGATTAGT	452
Qy	673	CAACCAAGTGGAAACAGCTAGCATTTCTCGCATCAATGGAAATCAGCAGAAATACTATCTGAG	732
Db	453	CATCAACCTGGACACTCAGTATTAATCCGTTCCATGGAAATCAGCACAGTATTACCAAGAG	512
Qy	733	AACAAATTGCCATGGCAGACGAGGGGATTAACATCGTAATGACAAACAGCTATCT	792
Db	513	AATAATCTTGCTCAAGCAGACGAGAAAGGTTATGATTAATTTGATGACAACTAGTCTGTCA	572
Qy	793	TCGGATGTTCTGTTGGATATTTTTCATGGCTGAGTATGATGATGACGACCGAGTGCAG	852
Db	573	TCAGGTGTTCTGTTGAGTATTTTTCATGGCGGAATATGATATTATGGCTCCAGTGCAA	632
Qy	853	CCGAAACTGAAGCTGCTCTTGACGCTGCTTTTCATTTCCAAATGTTGGTGTCTCGAAATTC	912
Db	633	CCAAAACAGAGAAAGCTCTTGCTGCTGCTTTTATTTTCCAAATTTGGCGCGCTCGAAATTTTC	692
Qy	913	CGTTTGAAGCTCTTGAGGCCCTTGA AAAAATCAAAACATCAAAAATTTGATTTCTTATGGTGT	972
Db	693	CGCTTGAAGCTCTTGAAGCCTTAATGAAGACGAATGTTAAGATTTGATTTCTTATGGTGT	752
Qy	973	TGTCACAGAACCTGTGATGGAAGAGTGAACAAAGTGAAGCCCTGAAGACTACAAATTT	1032
Db	753	TGTACACCGAATTCGGGATGGGAGTGTGGAGAGGTTGAGCTCTTAAGCACTACAAATTC	812
Qy	1033	AGCTTTAGCGTTTGA AAAATTCGAATGAGGAAGATTATGTAATCACTGAAAAATTTCTTCCAATCC	1092
Db	813	AGTCTAGCTTTTGAGACACCAACGAGGAGGATTTATGTCACAGAGAAGTTCTTCCAATCT	872
Qy	1093	CTTGTGTGGAACGTGCTCCCTGCTGTTGGTCTCTCAAATATTACGAGCTTTGCTCTCT	1152
Db	873	CTAGTCGCTGATCTGCTCCCTGCTGTTGGAGCTCCAAATATAGAAGAAATTTGCACT	932
Qy	1153	TCTCTGCTTCAATTTTACATATTAAAGAGATAGAGATGTGATGCTGTTGGCAAGACC	1212
Db	933	TCTCTGACTCATTCCTTCACATTAAGCAGATGATGATGTTCAAGGCAGTTGCAAGAA	992
Qy	1213	ATGAGATATCTAGCAGAAAAATCCCAAGCATATTAATCAATCATTTAGGTTGGAAGTATGAG	1272
Db	993	ATGAAGTATCTTGGGATACCCCTGACGCCTATTAATCAGACGCTAAGTGAAGACATGAA	1052
Qy	1273	GGTCATCTGACTCTCTCAAGGCCCTTGTGGATATGGCAGCTGTGCATTTCAATCTGTCCT	1332
Db	1053	GGCCCTTCAGATTCTTTTAAGGCATTTATTGATATGGCTGCTGTACACTCTTCTTGTCT	1112
Qy	1333	CTTTCGATTCATTGGCCACAGTGTAGTAGAGAGGAGNAANAATATCAAGCCTTTAAG	1392
Db	1113	CTCTGCATCTTTTGTGGCTTACAAGGATTCTGTGAGCAAGAGAGAGCCCTGAGTTTAAG	1172
Qy	1393	AGACGCTCTTGCAGTGCACCTAGAGGGCCAGAAAACCGTATATCATATCTATGTACAGAA	1452
Db	1173	AGACGACCTCGAAACGCCACAGGCTCAGACAGCTTTATCATTTGTATGTTAGAA	1232
Qy	1453	AGGGGAAGTTTGAGATGGAGTCCATTTTACTGAGGCTTAGCAATTTAACTCTGAATGCT	1512
Db	1233	AGAGGACGTTTTCATCGAATCCATCTTCTTGAAGGATGGAATCTGACTCTGGAAGCT	1292
Qy	1513	GTGAAGCTGCTGTTGTTTGAAGTTTCATCCCTGATCTTGTGCTGTATGCAAGACT	1572
Db	1293	CTGGAATCTGCGGTTCTTTCGGAAGTTTCATGTTCTCGAGATATGAACCAATATGAAGAAG	1352
Qy	1573	GAAAGCCTGAGTTTATGAAGGGGGAGTGCTTTTAAACCTCTCAAAAATATACCCAATT	1632
Db	1353	GAAAGCCCCGAGCTTAAGAGGAGACGGCAAGCTTAGAGTACATGGGATATATCTTAT	1412
Qy	1633	GGCTTGACACAGACAAGCTCTTTTATACCTTCAGCTTCAAAGTGTATGCTGATTCAGG	1692
Db	1413	GGTCTGACTCAAGACAGCTCTTTTACAACCTTCAAATTCGAAGGAAATTCAGTCTCAGT	1472
Qy	1693	AGTCACTTGGAGAACATCTCTTGCCCAAGTTTGAAGTCATTTTGTGTA	1742
Db	1473	ACTCATACAGAGAAACCCCTTGTCCTCAAAATTCGAAGTTGTCTTTGTCTA	1522
RESULT 10			
AY117132			
LOCUS	AY117132	1319 bp mRNA linear PLN 06-MAY-2005	
DEFINITION	Arabidopsis thaliana core alpha 1,3-fucosyltransferase mRNA, partial cds.		
ACCESSION	AY117132	GI:37545058	
VERSION	AY117132		
KEYWORDS	Arabidopsis thaliana (thale cress)		
SOURCE	Arabidopsis thaliana		
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.		
REFERENCE	1 (bases 1 to 1319)		

AUTHORS Kiefer-Meyer, M.-C., Faye, L. and Gomord, V.  
 TITLE Direct Submission  
 JOURNAL Submitted (03-JUN-2002) CNRS UMR 6037, Universite de Rouen, Mont Saint Aignan 76821, France  
 FEATURES  
 source 1. .1319  
 /organism="Arabidopsis thaliana"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:3702"  
 /clone="Ap47-33"  
 /ecotype="Wassilewskija"  
 <1. .1252  
 /EC\_number="2.4.1.214"  
 /codon\_start=2  
 /product="core alpha 1,3-fucosyltransferase"  
 /protein\_id="AAM77473.1"  
 /db\_xref="GI:37545059"  
 /translations="SGIEKQEWLERVDSVTSYRDTKDPITFSGNPKFKSCVSDCV  
 MGFSPDKPDAEPLGSHQPTLSIIRSMESAOYQENNLQAQRKGYDVMITSLSSD  
 VPGVYSWAEYDIMAIPQPKTEKALAAAFISNCAARFRLQALEALMKNVKNLDSYGG  
 CHNRDGSVEKVEALKHYPFLAFINNEEDYVTEKFFOSLVAGSVVVPVGNFIEEF  
 APSPDFLHIKQMDHDKVAKMKYLADNPDAVNTLRLWKHEGSPDSFKALIDMAVH  
 SSRLCIGIVATRIHEBEKSPKPCPKTRGSETVYHLYVRERGRFDMESIFLKDQ  
 NLTEALEGAVLAKFMSLRYEPTWKKERPASLRGDKLRVHGIYPIGLTORQALYNFK  
 FEGNSSLSITHIQRNPCPKFVFPV"  
 ORIGIN  
 Query Match 31.2%; Score 685.2; DB 15; Length 1319;  
 Best Local Similarity 71.8%; Pred. No. 2.7e-156;  
 Matches 897; Conservative 0; Mismatches 353; Indels 0; Gaps 0;  
 QY 493 TCTGAATCGTATAGTTGTGAGGAATGGTTGGAGGGAGGATGCTGTCAAGTATTCGAGG 552  
 DB 2 TCAGGAATAGAGAAATGCCAGGAGTGGTTAGAGAGAGTGGATTCACTTATTCTAGA 61  
 QY 553 GGCTTTTCCAAAGAGCCTATTTTGTCTTGGAGCTGATCAGGAGTGGAGTGGTTCG 612  
 DB 62 GATTTCATTAAGATCGATTTTATCTCTGGTAGTAAACAAGACTTCAAACTCGTCT 121  
 QY 613 GTTGGATGTAATTTGGGTTTGTGGGGATAGAAAGCCAGATCCGCAATTTGGTTACCT 672  
 DB 122 GTTGATTGTGAATGGGATTCACTTCAGATAAGAAACCTGATCGGCTTTGGATTAA 181  
 QY 673 CAACCAAGTGAACAGCTAGCATTTCTCGATCATCGAATCAGACAGATCTATCTGAG 732  
 DB 182 CATCAACCTGGAACACTCAGTATAATCCGTTCCATGGAATCAGACAGTATACCAAG 241  
 QY 733 AACATAATGCCATGGCAAGACGGAGGGATATAACATCGTAATGACCAACAGTCTATCT 792  
 DB 242 AATAATCTGCTCAAGCACACGCGAAGGTTATGATATTTGATGACNACTAGTCTGTCA 301  
 QY 793 TCGGATGTTCTGTGGATATTTTTCATGGGCTGAGTATGATATGATGGCAGGTCAG 852  
 DB 302 TCAGATGTTCTGTGGTATTTTTCATGGCGAATATGATATATGCTCCAGTCAA 361  
 QY 853 CGGAAACTGAAGTGTCTTGAGCTGCTTCAATTCGATGCTGCTGCTGCAATTC 912  
 DB 362 CCAAAAACAGAGAAAGCTTGTGTCGCGCTTTTATTTTCCAATTCGCGCGCTCGGAATTC 421  
 QY 913 CGGTTGCAAGCTTGTGAGGCGCTTGAANAATCAACATCAAAATTTGATTTGATGGTGT 972  
 DB 422 CGCTGCAAGCTTGTGAAGCTTAAAGACGATGTTAAGATTTGATTTGATGGTGT 481  
 QY 973 TGTCAAGGAACCGTGTATGGAAGTGAACAAAGTGAAGCCCTGGAAGCACTCAAAATTC 1032  
 DB 482 TGTCAAGGAATCGGATGGAGTGTGGAAGAGTTCGAAGCTCTTAAAGCACTCAAAATTC 541  
 QY 1033 AGCTTACGCTTGAATTCGAATGAGAGATTTATCTAATGAGAAATTTCTCCATCC 1092  
 DB 542 AGCTAGCTTTTGAGAACACCAACGAGGAGGATTTATGTCAGAGAAAGTTCTTCCAACT 601  
 QY 1093 CTTGCTGCTGGAACGTCCCTGTGGTGGTGGTCTCCAAATATTCAGGACTTTGCTCT 1152

DB 602 CTAGTCGTGGATCTGTCCCTGTGGTGTGTGGAGCTCCAAATATAGAAGAAATTTGCACCT 661  
 QY 1153 TCTCCTGTTCAATTTTACATATTAAGAGATAGAGGATGTTGAGTCTCTGTCAGAGACC 1212  
 DB 662 TCTCCTGATCTAATCTTCAATTAAGCAGATGGATGATGTCAAGGCAGTTGCAAGAAA 721  
 QY 1213 ATGAGATATCTAGCAGAAAATCCCGAAGCATATAATCAATCAATCAATGAGGTGGAAGTATGAG 1272  
 DB 722 ATGAAGTATCTTGGCGATAACCTGACGCTATATATCAGACCTAAGATGGAACATGAA 781  
 QY 1273 GGTCCATCTGACTCTTCAAGGCCCTTGTGGATATGGCAGCTGTGCAATTCATGTCGCCGT 1332  
 DB 782 GGCCCTTCAGATTCTTTAAGGCACTTATTGATATGGCTGTGTACACTCTTCTTCTCGT 841  
 QY 1333 CTTTGCATTCATCTGGCCACAGTGTAGAGAGAGGAGAGAAATATATCCAGCCCTTAAG 1392  
 DB 842 CTCTGCATCTTTGTGGCTACAAGGATTCATGAGCAAGAGAGAGAGCCCTGAGTTTAAG 901  
 QY 1393 AGACGTCCTTGAAGTGCACTAGAGGGCCAGAAAACCGTATATCATATCATATCTATGTACAGAA 1452  
 DB 902 AGACAACCTTGAATGCAACGAGGCTCAGAGACAGTTTATCATTTGTATGTAGAGAA 961  
 QY 1453 AGGGGAAGCTTTGAGATGGAGTCCATTTTACCTGAGGTCTAGCAATTTAACTCTGAATGCT 1512  
 DB 962 AGAGGACGGTTTGAATGCAATCCATCTTCTTGAAGGATGGAATCTGACTCTGGAAGCT 1021  
 QY 1513 GTGAGGCTGTCTGTTTGAAGTTCACATCCCTGAATCTTGTGCTCTGTATGGAAGACT 1572  
 DB 1022 CTGGAATCTGCGGTCTTCTCGAAGTTCATGCTCTGAGATATGAACCAATATGGAAGAG 1081  
 QY 1573 GAAAGCCTTGAAGTTATAGAGGGGGAGTGTCTTTAAAACTCTCAAAAAATATACCCAAAT 1632  
 DB 1082 GAAAGCCTGCGAGCTTAAAGAGAGACGCGCAAGCTTAGAGTACATCGGATATATCTTAT 1141  
 QY 1633 GGCTTGACACAGAGACAGCTCTTTATACCTTCAAGCTTCAAGGCTGATGCTGATTTTCAGG 1692  
 DB 1142 GGTCTGACTCAAAGCAAGCTCTTTTACAACCTTCAAAATTCGAAGGAAATTCAGTCTCAGT 1201  
 QY 1693 AGTCATCTGAGAACATCTTGTGCAAGTTTGAAGTCAATTTTCTGTGA 1742  
 DB 1202 ACTCATACAGAGAAACCTTGTCCCAAATTCGAAGTGTCTTCTGTCTA 1251  
 RESULT 11  
 ATH345085  
 LOCUS Arabidopsis thaliana mRNA for core-alpha1,3fucosyltransferase 2  
 DEFINITION (fucT2 gene).  
 ACCESSION AJ345085  
 VERSION AJ345085.1 GI:15722481  
 KEYWORDS core-alpha1,3fucosyltransferase 2; fucT2 gene.  
 SOURCE Arabidopsis thaliana (thale cress)  
 ORGANISM Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 Rosales; eurosids II; Brassicales; Brassicaceae; Arabidopsi.  
 REFERENCE 1  
 AUTHORS Bakker, H., Schijlen, E., de Vries, T., Schiphorst, W.E., Jordi, W.,  
 Lommen, A., Bosch, D. and van Die, I.  
 TITLE Plant members of the alpha1-->3/4-fucosyltransferase gene family  
 encode an alpha1-->4-fucosyltransferase, potentially involved in  
 Lewis(a) biosynthesis, and two core alpha1-->3-fucosyltransferases  
 FEBS Lett. 507 (3), 307-312 (2001)  
 JOURNAL 1169361  
 PUBMED 2 (bases 1 to 1542)  
 REFERENCE Bakker, H.  
 AUTHORS Direct Submission  
 TITLE Submitted (14-SEP-2001) Bakker H., Plant Research international,  
 Wageningen University and Research centr, droevendaalsesteeg 1,  
 Netherlands 6708PB, NETHERLANDS  
 JOURNAL Location/Qualifiers  
 FEATURES  
 source 1. .1542  
 /organism="Arabidopsis thaliana"







Db	744	GCTCGGAATTTTTCGTCTACAAGCAGCTTGGAGCAATTCATGAAAACTAACTTAAGATTGAT	803
Qy	961	TCTTATGGTGGTGTGTACAGGAACCGTGTATGGAAGAGTGAACAAAGTGGGAAGCCCTGAAG	1020
Db	804	TCTTATGGTGGTGTGTATCGAAACCGGAGTGGGAAAGTTGACAAAGTTGAAGCTCTTAAG	863
Qy	1021	CAGTACAAATTTAGCTTTAGCTTTGAAATTCGAAATGAGGAAGATTATGTAACCTGAAAAA	1080
Db	864	CGATACAAATTCAGTTTGGCTTTTGAATATCAACGAGGAAGATTATGTCACCGAGAAG	923
Qy	1081	TTCTTCCAAATCCCTTGTGTGCGAACTGTCCCTGTGGTGTGTGGTGCTCCAAATATTCAG	1140
Db	924	TTCTTTCAATCCCTTAGTTGCTGGTCCGTCCTCCGCTGGTAGTTGGTCTCCCAATATAGAA	983
Qy	1141	GACTTTGCTCTCTCTCGTTCATTTTACATATTTAAAGAGATAGAGGATGTGTAGTCT	1200
Db	984	GAAATTTGCGCTGCTTCGGACACATTCCTTCACATTAAGACTATGGAAGATGTAGAGCCA	1043
Qy	1201	GTTGCAAGACCATGAGATATCTAGCAGAAAAATCCCGAAGCATATATCAATCAATTCAGG	1260
Db	1044	GTTGCAAGAGAAATGAAGTATCTCGCAGCTAACCTCTGCTTATATATCAGACACTAAGA	1103
Qy	1261	TGGAAGTATGAGGGTCCATCTGACTCTCTTCAAGGCCCTTGTGGATATGGCAGCTGCAT	1320
Db	1104	TGGAATACAGGGTCTTTCAGATTCTTTCAGGCACTTGTTCATATGGCTGCTGTACAC	1163
Qy	1321	TCATCGTGGCGTCTTTGCAATTCATCTTGGCCACAGTGAGTAGAGAGGAAGAAAAATAAT	1380
Db	1164	TCCTTCTTGGCGTCTCTGCAATTTTCTGGCCACAGGGTCCGAGAACAAAGGAAGGAAAGT	1233
Qy	1381	CGAAGCCTTAAGAGACGTCTTCCGAAGT---GCACTAGAGGGCCAGAAACCGTATATCAT	1437
Db	1224	CCTAATTTCAAGAAACGACCGTGCNAATGTAGCAGGGGAGGATCAGACACAGTTTATCAT	1283
Qy	1438	ATCTATGTACAGAAAGGGGAAGGTTTGAGATGGAGTCCATTTACCTGAGGCTTAGCAAT	1497
Db	1284	GTTTTGTTAGAGAAAGAGCCGGTTTGAATGGAATCAGTCTTTTTGAGGGGTAAAAGT	1343
Qy	1498	TTAACTCTGAATGCTGTGAAGGCTGTGTTGTTTTGAAAGTTTCACATCCCTGGAATCTTGTG	1557
Db	1344	GTGACTCAGGAAGCTCTAGAATCTGCAAGTTCTGCAAGTTTCAAGTCTTTAAAAACATGAG	1403
Qy	1558	CTGTATGGAAGACTGAAGCCCTGAAGTTTAAAGAGGGGAGTGCTTTAAAACTCTAC	1617
Db	1404	GCAGTGTGGAAGAGGAAGGCCCTGGAAACTTTAAAGGAGACAAAGAGCTTTAAATACAT	1453
Qy	1618	AAATATACCAATTTGGCTTGACACAGAGCAAGCTCTTTATACCTTCAGCTTCAAAAGGT	1677
Db	1464	CGAATTTACCGCTTTGGCTTAACGCAACGACAGGCTTTGTACAACTTCAAAATTCGAGGA	1523
Qy	1678	GATGCTGAATTTACGAGGCTCACTTTGGAGAACAAATCCTTGTGCGCAAGTTTGAAGTCAATTTT	1737
Db	1524	AAATCGAGTCTAAGTAGTCACATTCAAAAACAAACCTTGTGCTAAATTTGAGGTGTCTCTC	158
Qy	1738	GTGTAG 1743	
Db	1584	GTCTAG 1589	
RESULT 13			
BT002570			
LOCUS			
DEFINITION	BT002570	1725 bp mRNA linear	PLN 20-DEC-2008
	Arabidopsis thaliana	Putative fucosyltransferase (At1g49710) mRNA,	
	complete cds.		
ACCESSION	BT002570		
VERSION	BT002570.1	GI:27311928	
KEYWORDS	FLI CDNA.		
SOURCE	Arabidopsis thaliana		
ORGANISM	Arabidopsis thaliana		
	(thale cress)		
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
	Arabidopsis thaliana		
	Eukaryota; Magnoliophyta; eudicotyledons; core eudicotyledons;		
	Spermatophyta; Magnoliopsida; Brassicales; Arabidopsidaceae; Arabidopsis		
	rosidae; eurosids II; Arabidopsidaceae; Arabidopsidaceae; Arabidopsidaceae;		

REFERENCE  
AUTHORS

1. (bases 1 to 1725)  
 Nguyen,M., Southwick,A., Tripp,M., Palm,C.J., Jones,T., Wu,T.,  
 Carninci,P., Chen,H., Cheuk,R., Chan,M.M., Chang,C.H., Dale,J.M.,  
 Deng,J.M., Hayashizaki,Y., Hsuan,V.W., Lee,J.M., Ishida,J.,  
 Kamiya,A., Kawai,J., Kim,C.J., Narusaka,M., Onodera,C.S.,  
 Quach,H.L., Sakurai,T., Satou,M., Seki,M., Shinn,P., Tang,C.C.,  
 Toroumi,M., Wong,C., Wu,H.C., Yamada,K., Yu,G., Yuan,S.,  
 Shinzaki,K., Ecker,J., Theologis,A. and Davis,R.W.  
 Direct Submission  
 Submitted (20-DEC-2002) DNA Sequencing and Technology Center,  
 Stanford University, 855 California Avenue, Palo Alto, CA 94304,  
 USA  
 e-mail for correspondence: arab@sequence.stanford.edu

COMMENT

RIKEN Genomic Sciences Center (GSC) members carried out the  
 collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN  
 Arabidopsis Full-Length cDNA'): Seki,M., Narusaka,M., Ishida,J.,  
 Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J.,  
 Hayashizaki,Y. and Sh inozaki,K.

The Salk, Stanford, PGEC (SSP) Consortium members carried out the  
 sequencing and annotation of the RAFL cDNAs: Nguyen,M., Tripp,M.,  
 Southwick,A., Palm,C.J., Jones,T., Wu,T., Chen,H., Cheuk,R.,  
 Chan,M.M., Chang,C.H., Dale,J.M., Deng,J.M., Hsuan,V.W., Lee,J.M.,  
 Kim,C.J., Quach,H.L., Onodera,C.S., Shinn,P., Tang,C.C.,  
 Toroumi,M., Wong,C., Wu,H.C., Yamada,K., Yu,G., Yuan,S., Ecker,J.,  
 Theologis,A. and Davis,R.W.

Nguyen,M., (SSP/Stanford) and Seki,M. (RIKEN GSC) contributed  
 equally to this work. Shinzaki,K. (RIKEN GSC) and Davis,R.W.  
 (SSP/Stanford) contributed equally to this work as PIs.

FEATURES  
source

Location/Qualifiers  
 1..1725  
 /organism="Arabidopsis thaliana"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:3702"  
 /chromosome="1"  
 /clone="U16327"  
 /ecotype="Columbia"  
 /note="This clone is in pENTR/SD-dTopo This is a cloned  
 PCR product using RIKEN clone RAFL07-14-009 (AY054522) as  
 a template"  
 1..1725  
 /gene="At1g49710"  
 /note="synonym: F14J22.8"  
 1..1542  
 /gene="At1g49710"  
 /codon\_start=1  
 /product="Putative fucosyltransferase"  
 /protein\_id="AA00930.1"  
 /db\_xref="GI:27311929"  
 /translation="MGVFSNLRGPRAGATHDEFPATNGSPSSSPSSSIKRLNLL  
 PLVALVIAETGFLGRDLKVALVDTLDTFTQSPSLQSPAPSDRKKIGLFTDRSC  
 EWLMLREDSVTVSRDTPDPIFISGKEDQFOWCVDCTFGDSGKTPOAFLGLGKPG  
 TLIIRSMESAGYYPENDLAQARRGYDVMITSLSDVPVGFYFSAEVDIMSPVQPK  
 TERATAAPFISNGCARFRLQALRMKTNIKIDSYGCHNRDCKDKVLAKEYKF  
 SLAFENTDEEDYVTEKFFQSLVAGSPVVPVPPNIEEPAPASDFSLHITMEDVEPVA  
 KMKYLAAPNAYNOTLRWKYEGDSFKALVDMVAHSSCRLCIFLATRVREDEES  
 PNFKRCPKCSGGSDTVVHVFVRERGFEMESVFLRGKSVTOEALESVILAKFKSLK  
 HEAVNKKERPGNLKGDKELKIHRIYPLGLTQRLQALYNFKFEGNSLSLSHHIQNNPCAKF  
 EVFV"

gene

CDS

ORIGIN

Query Match 30.9%; Score 678.8; DB 15; Length 1725;  
 Best Local Similarity 68.4%; Pred. No. 9.8e-155;  
 Matches 989; Conservative 0; Mismatches 442; Indels 15; Gaps 3;  
 301 AAGAGAAATGAGCAATCAATGCTCTTGTGTTGCCCTTGTGCTATCCGAGATC 360  
 109 AAGCGAAAATATCGAATTTGTTACCACTCTCGTGTGCTCTGCTGCTGAGATC 168  
 361 GCGTTTCTGGTAGGTGGATATGCGCAAAACGCCCATGCTTACCTCCCTCGCTGAC 420

169 GGGTTTCTGGTCCGCTCGAT-----AAAGTCGCTTTGGTTGATACGTTGACTCAT 219  
 421 TTCTTCTACCGCTCTCCAGCGGTGTTGAAGGTGACGATTTCGGTTTGGGTTTGGTGGCT 480  
 220 TTCTTCCACCAAGTCTCCGTCACTCTCCAGTCTCCACGGCGAGATCCGATCGGAAGAAG 279  
 481 TCTGATCGGAATTCGAATCGTATAGTGTGAGGAATGTTGGAGAGAGGAGGATGCTGTC 540  
 280 ATCGGATTAATTACTGATAGS---AGTCGCGAGGAGTGGTTGATGAGAGAAGATTCAGTT 336  
 541 ACGTATTCGAGGGGCTTTCCAAAGAGCGCTATTTTGTGTTCTGAGCTGATCAGAGTGG 600  
 337 ACTTACTCTAGAGATTTTACTAAAGATCCAAATTTTATCTCTGCTGGTGAAGAGACTTT 396  
 601 AAGTCGTTTCGGTTCGATGTAAATTTGGGTTTGTAGTGGGATACAAAGCCAGATGCCCA 660  
 397 CAATGGGTGTTCTGGGATGTTGACATTTGGAGATAGTTTCAGGGAANAACACAGATGCTGCG 456  
 661 TTTGGGTTACCTCAACCAAGTGGAAACAGCTAGCATCTTCGCGATCAATGGAAATCAGCAAA 720  
 457 TTTGGATAGTCAAGAACCTCGAACTCTTAGTATATAATACGTTCCATGGAAATCAGCACAG 516  
 721 TACTATGCTGAGAAACAATATTGCCATGGCAAGACGAGGGGATATAACATCGTAAATGACA 780  
 517 TATTATCCAGAAAATGATCTTTGCAACAGCGACGACGAGAGGTTATGATATAGTAGTAC 576  
 781 ACCAGTCTATCTCGGATGTTCTGTTGGATATTTTTCATGGGCTGAGTATGATATGATG 840  
 577 ACTAGTCTATCATCAGATGTTCTGTTGGATATTTTTCGTTGGGAGGATGATGATATGATG 636  
 841 GCACAGTGCAGCGCAAAACCTGAAAGCTGCTCTTCGAGCTGCTTTCAITTTCCAAATTTGGT 900  
 637 TCTCGGTACAGCAAAAACCTGAGAGAGCTATTCAGCTGCTTTTATTTTCTAATTTGCT 696  
 901 GCTCGAAATTTCCGGTTCCAAAGCTCTTCGAGCCCTTCGAAAAATCAAAACATCAAAATTCAT 960  
 697 GCTCGAAATTTTCGTTCTACAAGCACTTGAGGCACTTGAGAACTAACTAACTAAGATTGAT 756  
 961 TCTTATGTTGTTGCTGCACAGAAACCGTGTAGGAGAGTGAACAAAGTCGAAGCCCTGAAG 1020  
 757 TCTTATGTTGTTGTTGTCATCGAAACCGGATGGGAAAGTTGAAAGTTGAAGCTCTTAAG 816  
 1021 CACTACAAATTTAGCTTAGCTTACCGTTTCAAAATTCGAATGAGGAGATTTATGTAACCTGAAA 1080  
 817 CGATACAAATTCAGTTTGGCTTTTGAAGATATACTAACGAGGAAGATTATGTCAACGAGA 876  
 1081 TTCTTCCAAATCCCTTGTGCTGGAACATGTCCTCGTGTGTTGTTGCTGCTCAAAATATTGAC 1140  
 877 TCTTTTCAATCCTTAGTTGCTGGGTCCGTCCTCCGCTGGTGTAGTTGGTCTCTTCCAAATATAG 936  
 1141 GACTTGTCTCTCTCTGTTTCAATTTTACATATTAAGAGATAGAGGATGTTGAGTCT 1200  
 937 GAATTTGCGCTGCTTCCGACTCAATCTCTTCACTAATAGACTATGGAAGATGTAAGACCA 996  
 1201 GTTCAAGAGACATGAGATATCTAGCAGAAAATCCGAAAGCATATAATCAATCAATTTGAGG 1260  
 997 GTTCAAGAGAAATGAAGATCTTCGAGCTAACCTGCTGCTTATATCAGACACTAAGA 1056  
 1261 TGGAGATGAGGGTCCATCTGATCTCTTCAAGGCCCTTTGGGATATATGGCAGCTGTGATC 1320  
 1057 TGGAAATACGAGGGTCTCTTCAAGTCTTTTCAAGGCACCTTTGTTGATGATGCTGCTGTACAC 1116  
 1321 TCATCGTCCGCTCTTTCGATTTCACTTGGCCACAGTGTAGTAGAGAGAGAGAAATAAT 1380  
 1117 TCTTCTTGGCCGCTCTGCGATTTTCTGGCCACAGGGTCCGAGAAACAAGAGAGAGAAAGC 1176  
 1381 CCAGCCCTTAAGAGAGCTCTTGCAGAGT---GCACCTAGAGGCCCAAGAAACCGTATATCAT 1437  
 1177 CTAATTTCAAGAAACGACCGTGCAAATGTAGCGGAGGATCAGACACAGTTTATCAT 1236  
 1438 ATCTATGTCAGAGAAAGGGAGGTTTCAGATGAGAGTCCATTTTACCTGAGGCTTAGCAAT 1497  
 1237 GTTTTGTAGAGAAAGGCGCGTTCGAAATGGAATCAGTCTTTTTCGAGGGTAAAAAGT 1296

QY	1498	TTAACTCTGAATCTGTGAAGGCTGCTGTTGTTTGAAGTTCATCCTCCTGAATCTTGTC	1557	/gene="At1g49710; F14J22.8"
Db	1297	GTGACTCAGGAAGCTCTAGAATCTGCAGTCTCGCAAGTCTCAAGTCTTTAAACATGAG	1356	160..1701
QY	1558	CGTGATGGAAGACTGAAAGGCTGAAGTTTATAAGAGGGGGAGTCTTTAAACCTCTAC	1617	/gene="At1g49710; F14J22.8"
Db	1357	GCAGTGTGGAAGAAGGAAGGCTCGAACTTAAAGGAGCAAGAGCTTAAATACAT	1416	/codon_start=1
QY	1618	AAAATATACCAATTTGGCTTTGACACAGACAAGCTCTTTTATACCTTCAGCTTCAAAGT	1677	/product="Putative fucosyltransferase"
Db	1417	CGGATTTACCGCTTGGCCTTAACGCAACGACAGCTTTGTACAACTTCAAACTCGAGGGA	1476	/protein_id="AAK96713.1"
QY	1678	GATGCTGATTTCAAGGAGTCACTTGGAGAACATCTCTTGTGCGCAAGTTGAAGTCATTTT	1737	/db_xref="GI:15450884"
Db	1477	AAATCGAGTCTAAGTAGTCACATTCAAATCAAAACACCTTGTGCTAAATTTGAGGTTGCTTC	1536	/translation="MGVFNLRGPRAGATHDEFPATNGSPSSSSSSSSSIKRLNL
QY	1738	GTCTAG 1743		PLCVLVVIAIGELGRDLKVALVDLTLDFTQSPSLSQSPARDRKKGILGFTDRSC
Db	1537	GTCTAG 1542		BEWLMRESVYSRDFDKDPIFISGGEKDFQWCSVDCTFGDSSGGTDPDAAGLGKQPG
RESULT 14				
AY054522				
LOCUS				
DEFINITION				
Arabidopsis thaliana Putative fucosyltransferase (At1g49710;				
F14J22.8) mRNA, complete cds.				
ACCESSION				
AY054522				
VERSION				
AY054522.1 GI:15450883				
KEYWORDS				
FLI CDNA.				
SOURCE				
Arabidopsis thaliana (thale cress)				
ORGANISM				
Arabidopsis thaliana				
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;				
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.				
1 (bases 1 to 1938)				
Southwick,A., Karlin-Neumann,G., Nguyen,M., Lam,B., Miranda,M.,				
Palm,C.J., Bowser,L., Jones,T., Banh,J., Carninci,P., Chen,H.,				
Cheuk,R., Chung,M.K., Hayashizaki,Y., Ishida,J., Kamiya,A.,				
Kawai,J., Kim,C., Lin,J., Liu,S.X., Narusaka,M., Pham,P.K.,				
Sakano,H., Sakurai,T., Satou,M., Seki,M., Shinn,P., Yamada,K.,				
Shinozaki,K., Ecker,J., Theologis,A. and Davis,R.W.				
Direct Submission				
Submitted (28-AUG-2001) DNA Sequencing and Technology Center,				
Stanford University, 855 California Avenue, Palo Alto, CA 94304,				
USA				
e-mail for correspondence: arab@sequence.stanford.edu				
RIKEN Genomic Sciences Center (GSC) members carried out the				
collection and clustering of RAFL cDNAs (RAFL cDNA: "RIKEN				
Arabidopsis Full-Length cDNA": Seki,M., Narusaka,M., Ishida,J.,				
Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J.,				
Hayashizaki,Y. and Shinozaki,K.				
The Salk, Stanford, PDEC (SSP) Consortium members carried out				
sequencing and annotation of the RAFL cDNAs: Nguyen,M.,				
Southwick,A., Karlin-Neumann,G., Lam,B., Miranda,M., Palm,C.J.,				
Bowser,L., Jones,T., Banh,J., Chen,H., Cheuk,R., Chung,M.K.,				
Kim,C., Lin,J., Liu,S.X., Pham,P.K., Sakano,H., Shinn,P.,				
Yamada,K., Ecker,J., Theologis,A. and Davis,R.W.				
Southwick,A., (SSP/Stanford) and Seki,M. (RIKEN GSC) contributed				
equally to this work. Shinozaki,K. (RIKEN GSC) and Davis,R.W.				
(SSP/Stanford) contributed equally to this work as PIs.				
Location/Qualifiers				
1..1938				
/organism="Arabidopsis thaliana"				
/mol_type="mRNA"				
/db_xref="taxon:3702"				
/chromosome="1"				
/clones="RAFL07-14-009"				
/note="This clone is in pBluescript"				
1..1938				
gene				
ORIGIN				
Query Match				
Best Local Similarity				
Matches				
30.9%; Score 678.8; DB 15; Length 1938;				
68.4%; Pred. No. 9.8e-155;				
0; Mismatches 442; Indels 15; Gaps 3;				
QY	301	AAGAGGAATGAGCAATCTAATGCCTCTTGTGTGTCCTTGTGGTCAATCGCGGAGATC	360	
Db	268	AAGCGAAATATTGCAATTTGTTACCACTCTCGTTCGTCTGTAGTTATCGCTGAGATC	327	
QY	361	GGCTTTCTGGTAGTGGATATGCCAAAACCGCGCATGTTGACTCCCTCGCTGAC	420	
Db	328	GGGTTTCTGGGTCGGCTCGAT-----AAAGTCGCTTTGGTTGATACGTTGACTGAT	378	
QY	421	TTCTTCTACCGCTCTCGAGCGGTGTTGAAGGTGACGATTTGGGGTTGGGTTTGGTGGCT	480	
Db	379	TTCTTCAACCACTCTCCGTCACCTCTCGAGTCTCCACCGCGGAGATCCGATCGGAAGAAG	438	
QY	481	CTGTGATCGGAATTTCTGAATCGTATAGTTGTGAGGAATGTTGGAGAGGAGGATGCTGTC	540	
Db	439	ATCGGATTTATTTACTGATAGG--AGCTCGAGGAGTGGTTGATGAGAGAAGATTGAGTT	495	
QY	541	AGTATTCAGGGGCTTTTCCAAAGAGCTATTTTGTCTTCTGGAGCTGATCAGGAGTGG	600	
Db	496	ACTTACTCTAGAGATTTTACTAAAGATCCAAATTTTATCTCTGGTGGTGAAGAGGACTTT	555	
QY	601	AACTGCTGTTCTGGTGGATGTAATTTTGGGTTTAGTGGGGATAGAAAGCCAGATGCCGA	660	
Db	556	CAATGCTGTTCTGGGATTTGATTTGGAGATGTTTCAGGGAAACACACAGATGCTGCG	615	
QY	661	TTTGGTTACCTCAACCAAGTGGAACTGCTAGCATTTCTCGATCAATGGAATCAGCAGAA	720	
Db	616	TTTGGATTAGTTCAGAAACCTTGAACCTTTAGTATTAATACGTTCCATGGAATCAGCACAG	675	
QY	721	TACTATGCTGAGAACCAATATTCGCATGGCAAGCGGAGGGATATACATCGTAAATGACA	780	
Db	676	TATTATCCGAAATATGATCTTGCACAGCAGCAGGAGGTTATGATATAGTATGATGACC	735	
QY	781	ACCAGTCTATCTCGGATGTTCTGTTGGATATTTTTTCATGGGCTCAGTATGATATGATG	840	
Db	736	ACTAGTCTATCATCATGATGTTCTGTTGGAATATTTTCTGGCGGAGTATGATATATG	795	
QY	841	GCACCAAGTCAGCGCGGAAACTGAAAGCTGCTCTTTCAGAGTCTGTTTCAATTTGCGGT	900	
Db	796	TCTCCGTCAGCGCAAAACTGAGAGAGCTATTGCGAGCTGCTTTTATTTCTAAATTTGGT	855	
QY	901	GCTCGAAATTCGCGTTGCAAGCTCTTGAGGCCCTTGAAAAATCAACATCAAAATGAT	960	
Db	856	GCTCGGAAATTTGCTCTACAAAGCATTGAGGCAATGATGAAAACTAACATTAAGATTGAT	915	
QY	961	TCTTATGCTGTTGTTCACAGGAACCGCTGATGGAAGAGTGAACAAAGTGAAGCCCTCAAG	1020	
Db	916	TCTTATGCTGTTGTCTATCGAAACCGGATGGGAAGTTGACAAGTTGAGGCTCTTAAG	975	
QY	1021	CACACAAATTTAGCTTAGCGTTTGAAATTCGAATGAGGAAGATTATGTAACCTGAAAAA	1080	

Db 976 CGATACAAATTCAGTTTGGCTTTTGGAGATATTAACAGGAAGATTATGTCACCGAGAAG 1035  
Qy 1081 TTCTTCCAAATCCCTTGTGCTGGAACTGTCCCTGTGTTGGTGTCTCAAATATTCAG 1140  
Db 1036 TTCTTCCAAATCCCTTGTGCTGGGTCGTCCTCCGTCGTGTGTTGGTCTCCAAATATAGAA 1095  
Qy 1141 GACTTTTCTCTCTCTCTCTCTCTCAATTTTACATATTAAGAGATAGAGGATGTTGAGTCT 1200  
Db 1096 GAATTTGCGCTGCTTCCGACTATCTCTTACATTAAGACTATGGAAGATGTAGAGCCA 1155  
Qy 1201 GTTGCAAGACCAATAGATATCTAGCAGAAAATCCGAAAGCATATAATCAATCAATGAGG 1260  
Db 1156 GTTGCAAGAGATGAAGTATCTGCAGCTAAACCTGCTGCTTATAATCAGACACTAAGA 1215  
Qy 1261 TGGAGTATGAGGTCATCTGACTCTTCAAGCCCTTGTGATATGCGAGCTGTGCAT 1320  
Db 1216 TGGAAATACAGGGTCCTTCAGATTCTTCAAGGCACCTTGTGATATGCGTGTGTACAC 1275  
Qy 1321 TCATCGTGGCTCTTTCGATTCATCTTGGCCACAGTGAGTAGAGAGGAAGAAAATAAT 1380  
Db 1276 TCCTTTGCGCTCTCTGCAATTTCTGCGCCACAGGGTCCGAGAACAGAGAGGAAGC 1335  
Qy 1381 CCAAGCCTTAAGAGACGTCCTTGAAGT---GCACTAGAGGGCCAGAAACCGTATATCAT 1437  
Db 1336 CCTAATTTCAAGAACCGCTGCAATGTAGCAGGGGAGGATCAGACACAGTTTATCAT 1395  
Qy 1438 ATCTATGTCAGAGAAAGGGAGGTTTGAGATGAGTGCATTTACCTGAGGTCTAGCAAT 1497  
Db 1396 GTTTTCTGTAGAGAAAGGCGGTTTGAATGGAATCAGTCTTTTGGAGGGTAAAGT 1455  
Qy 1498 TTAACCTGAGTCTGTGAGGCTGCTGTTGTTTGAAGTTTCAATCCCTGAACTTTGTG 1557  
Db 1456 GTGACTCAGGAAGCTCTAGAACTGCAAGTCTCCGCAAGTTTCAAGCTTTTAAACATGAG 1515  
Qy 1558 CCTGTATGGAAGACTGAAGGCTGAAAGTTTATAAGAGGGGGAGTGTCTTTAAAACTCTAC 1617  
Db 1516 GCAGTGTGAAGAGGAAGGCTGGAAGCTTAAAGAGAGACAAGAGCTTAAATACAT 1575  
Qy 1618 AAAATATACCAATTTGGTTGACACAGAGCAAGCTCTTTATACCTTCAGCTTCAAAGGT 1677  
Db 1576 CGGATTTACCGCTTGGCTTAAACGACAGCAGAGGCTTTGTACAACTTCAAATTCAGGGA 1635  
Qy 1678 GATCTGATTTACGAGTCTCCTGAGAACAACTCTGTGCAAGTTTGAAGTCAATTTT 1737  
Db 1636 AATTGAGTCTAAGTAGTCAATCAAAACAAACCTTTGTGCTAAATTTGAGGTTGTCTTC 1695  
Qy 1738 GTGTAG 1743  
Db 1696 GTCTAG 1701

RESULT 15  
LOCUS AV184991 1568 bp mRNA linear PLN 02-MAR-2005  
DEFINITION Arabidopsis thaliana alpha 1, 3-fucosyltransferase-like protein  
mRNA, complete cds; alternatively spliced.  
ACCESSION AV184991  
VERSION AV184991.1 GI:37731911  
KEYWORDS  
SOURCE Arabidopsis thaliana (thale cress)  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopses.  
1 (bases 1 to 1568)  
Kiefer-Meyer M.-C., Faye, L. and Gomord, V.  
Direct Submission  
Submitted (21-NOV-2002) CNRS UMR 6037, Universite de Rouen,  
Batiment Extension Biologie, Mont Saint Aignan 76821, France  
Location/Qualifiers  
FEATURES  
source  
1. 1568  
/organism="Arabidopsis thaliana"  
/mol\_type="mRNA"

/db xref="taxon:3702"  
/ecotype="Wassilewskija"  
5..571  
/note="alternatively spliced"  
/codon\_start=1  
/product="alpha 1, 3-fucosyltransferase-like protein"  
/protein\_id="AA064481.1"  
/db\_xref="GI:37731912"  
/translation="MGVFNLRGRPRAGATHDEFPATNGSPSSSSSSSSSKIKLSNLL  
PLCALVVAIEIGFLRLDKVALVDLTTPFTQPSLSQSPPARSDRKKIIGLFTDRSC  
EWMREDSVTVSRDFTKDPIDFISGEEDFQWCVDTFGDSSGKTPDAAPGLGQKPG  
TUSIIRMSBQAQYCPENDLQAARRWERL"  
ORIGIN  
Query Match 30.2%; Score 664.8; DB 15; Length 1568;  
Best Local Similarity 68.2%; Pred. No. 2.6e-151;  
Matches 989; Conservative 0; Mismatches 442; Indels 19; Gaps 4;  
Qy 301 AAGAGAAAATGGAGCAATCTAATCCCTCTTGTGTTGTCCTCTGTGGTCAATCGCGAGATC 360  
Db 113 AAGCGAAAATATCGAATTTGTTACCACTCTGCGTTGCTCTGGTAGTTATCGCTGAGATC 172  
Qy 361 GCGTTTCTGGGTAGGTTGGATATGGCCAAAAGCCGCCCATGGTTGACTCCCTCGCTGAC 420  
Db 173 GGGTTTCTGGGTGGCTCGAT-----AAAGTCGCTTTGGTTGATACGTTGACTGAT 223  
Qy 421 TTCTTCTACCGCTCTCGAGCGGTCGTTGAAGGTGACGATTTGGGGTTGGGTTGCTGGCT 480  
Db 224 TTCTTCAACCGAGTCTCCGTCCTCGCATCTCCACCGCGAGATCCGATCGGAAGAG 283  
Qy 481 TCTGATCGGAATTTCTGAATCGTATAGTTGTGAGGAATGGTTGGAGAGGGAGGATGCTGTC 540  
Db 284 ATCGGATTTATCTGATAGG---AGCTGCGAGGAGTGGTTGATGAGAGAAGATTCAATT 340  
Qy 541 ACGTATTCGAGGGCTTTTCCAAAGACCTATTTTCTGTTGTTGTTGTTGTTGTTGTTGTTG 600  
Db 341 ACTTACTCTAGAGATTTTACTAAAGATCCAAATTTTATCTCTGTTGTTGTTGTTGTTGTT 400  
Qy 601 AAGTCGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 660  
Db 401 CAATGGTGTCTGTGGATTTGATTTGGAGATAGTTTCAGGGAACACACAGATGCTGCG 460  
Qy 661 TTTGGGTACTCTCAACCAAGTGGAACTAGTCTGCAATCTGCGATCAATGGAAATCAGAGAA 720  
Db 461 TTTGGATAGTTCAGAAACCTGGACTCTTAGTATATATACGTTCCATGGAAATCAGACAG 520  
Qy 721 TACTATGCTCAGAACCAATATTTGTCATGCGCAAGACGAGG---GGATATACATCTGTAAT 776  
Db 521 TATTTGCCAGAAAATGATCTTGCACAGGCACGCGTGGGAGAGGTTTATGATATAGTAT 580  
Qy 777 GACAAACAGTCTATCTTCGGATGTTCTGTTGGATATTTTTCATGGGCTGAGTATGATAT 836  
Db 581 GACCACATGATCTATCATCAGATGTTCTGTTGGATATTTTTCGTTGGGCGGAGTATGATAT 640  
Qy 837 GATGGCACCATGTCAGCGCGGAAACTGAAAGCTGCTTCTTCAGCTGCTCTTTCATTTCCAAAT 896  
Db 641 TATGTCCTCCGTACAGCCAAACCTGAGAGAGCTATTTGACGCTCTTTTATTTCTTAATG 700  
Qy 897 TGGTGTCTGAAAATTTCCGGTTGCAAGCTCTTGGAGGCTTTGAAAATCAAAATCAAAAT 956  
Db 701 TGGTGTCTGGAATTTTCTCTACAAGCACTTGAAGCATTTGATGAAAATCAACATTAAGAT 760  
Qy 957 TGATTTCTTATGGTGGTTGTCACAGAACCGTGTAGGAGAGTGAACAAAGTGAAGCCCT 1016  
Db 761 TGATTTCTTATGGTGGTTGTCATCAAAACCGGAGTGGGAAAGTTGACAAAGTTTGAAGCTCT 820  
Qy 1017 GAAGCACTACAAATTTTAGCTTAGGCTTTGAAAATTTGAAATTCGAATCAGGAAGATTTATGTA 1076  
Db 821 TAAACGATACAAATTTAGTTGGCTTTTGGATTAATCTAAACGAGGAAGATTTATGTCACCGA 880  
Qy 1077 AAAATTTCTTCAATCCCTTGTGCTGGAAGTGTCCCTGTGGTGTGTTGTTGTTGTTGTTGTT 1136  
Db 881 GAAGTTCTTCAATCCCTTGTGCTGGTTCGTTCCCGTGGTAGTTGTTGTTGTTGTTGTTGTT 940



Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	2198	100.0	2198	3	AAA97937	Mung bean
2	664.8	30.2	2036	13	ADT15744	Adt15744 plant cDN
3	661.6	30.1	1982	3	AAC39529	Arabidops
4	657	29.9	1790	13	ACN62531	Plant fun
5	245.2	11.2	650	13	ACN54249	Cotton an
6	209.4	9.5	2069	4	AAF84907	Nitrogen-
7	209.4	9.5	2124	4	AAF84910	Asf84910 Nitrogen-
8	209.4	9.5	2165	4	AAF84913	Nitrogen-
9	209.4	9.5	2232	4	AAF84916	Nitrogen-
10	209.4	9.5	2808	4	AAF84906	Nitrogen-
11	209.4	9.5	2863	4	AAF84909	Nitrogen-
12	209.4	9.5	2904	4	AAF84912	Nitrogen-
13	209.4	9.5	2971	4	AAF84915	Nitrogen-
14	209.4	9.5	3714	4	AAF84905	Nitrogen-
15	209.4	9.5	3775	6	AD38881	Alfalfa A
16	145.8	6.6	567	13	ACN53160	Cotton an
17	105	4.8	105	3	AA97938	Mung bean
18	86.2	3.9	810	13	ADX53170	Plant fun
19	84.2	3.8	287	6	ABL76406	Corn tass

This invention describes a novel DNA molecule (1), encoding a plant CC protein with fucosyl transferase activity, GlcNAc- $\alpha$ -1,3-fucosyl CC transferase. The methods and DNA sequences are useful for production of CC recombinant GlcNAc- $\alpha$ -1,3-fucosyltransferase. The enzyme is useful for CC the production of recombinant human glycoproteins, which are especially CC





Db 1981 AGTCACAGTCTCTGTATATTGTGAGTCAAACTGAAATCTAATAGAGGATCAGATGTTT 2040  
QY 2041 CACTCAAGACACATTATTACTTCATGTTGTTTGTATGATCTCAGCTTTTATTAGTCTG 2100  
Db 2041 CACTCAAGACACATTATTACTTCATGTTGTTTGTATGATCTCAGCTTTTATTAGTCTG 2100  
QY 2101 GAATGTCCTCTGTTGTTGAGCACCTGTTATTGCTTCAGTGTACTGTCAGTGGTTATC 2160  
Db 2101 GAATGTCCTCTGTTGTTGAGCACCTGTTATTGCTTCAGTGTACTGTCAGTGGTTATC 2160  
QY 2161 GTTTTGGACCTCTAATAAAAAAAAAAAAAAAAAAAAAA 2198  
Db 2161 GTTTTGGACCTCTAATAAAAAAAAAAAAAAAAAAAAAA 2198

RESULT 2

ADT15744  
ID ADT15744 standard; cDNA; 2036 BP.

AC ADT15744;

DT 13-JAN-2005 (first entry)

DE Plant cDNA, Seq ID 1070.

XX Plant; ss; gene; transgenic; cold tolerance; growth rate;

KW drought tolerance; disease resistance; galactomannan production;

KW plant growth regulator; heat tolerance; herbicide tolerance;

KW lignin production; extreme osmotic condition tolerance;

KW pathogens resistance; pest resistance; yield improvement; seed oil yield;

KW seed protein yield.

XX Viridiplantae.

OS US2004216190-A1.

PN 28-OCT-2004.

XX 18-DEC-2003; 2003US-00739930.

XX 28-APR-2003; 2003US-00424599.

PR 28-APR-2003; 2003US-00425115.

XX (KOVA/) KOVALIC D K.

PA Kovalic DK;

XX WPI; 2004-757369/74.

XX New recombinant DNA constructs useful in the field of biochemistry and genetics, and in particular for producing transgenic plants with improved biological characteristics.

PS Claim 1; SEQ ID NO 1070; 14pp; English.

CC The invention relates a recombinant DNA construct comprising a polynucleotide having any of 5544 nucleotide sequences (cDNAs SEQ ID NO: 1-5544) and encoding a polypeptide with any of 5544 amino acid sequences (SEQ ID NO: 5545-11088). The cDNAs and proteins are from corn, soybean, Arabidopsis, wheat and rape but the specification does not indicate which sequences is derived from which organism. Also included is a method of producing a plant having an improved property, comprising transforming a plant with a recombinant DNA construct comprising a promoter region functional in a plant cell operably joined to a polynucleotide encoding a polypeptide associated with the property, and growing the transformed plant. The property is selected from improving plant cold tolerance, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for improving plant drought tolerance, for providing increased resistance to plant disease, for galactomannan production, for production of plant growth regulators, for improving plant heat tolerance, for improving plant tolerance to herbicides, for increasing the rate of homologous recombination in plants, for lignin production, for improving

CC plant tolerance to extreme osmotic conditions, for improving plant tolerance to pathogens or pests, for yield improvement by modification of photosynthesis, for modifying seed oil yield and/or content, for modifying seed protein yield and/or content, for yield improvement by modification of carbohydrate, nitrogen or phosphorus use and/or uptake and for yield improvement by providing improved plant growth and development under at least one stress condition. The polynucleotide may also encode a plant transcription factor. The methods and compositions of the present invention are useful in the field of biochemistry and genetics, in particular for producing transgenic plants with improved biological characteristics such as increased yield, improved nitrogen flow, increasing plant tolerance to cold or heat, improving plant tolerance to extreme osmotic and drought conditions, and improving plant tolerance to plant pests or pathogens. They can also be used in physical arrays of molecules, plant breeding markers, computer-based storage and analysis systems. The present sequence is one of the 5544 plant cDNA sequences of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html?DocID=20040216190.

XX Sequence 2036 BP; 596 A; 392 C; 446 G; 602 T; 0 U; 0 Other;

QY Query Match 30.2%; Score 664.8; DB 13; Length 2036;

Db Best Local Similarity 68.2%; Pred. No. 1.1e-166;

XX Matches 989; Conservative 0; Mismatches 442; Indels 19; Gaps 4;

QY 301 AAGAGGAATCGAGCAATCTAATGCTCTTGTGTTGCTCTGTCATCGCGGAGATC 360

Db 268 AAGCGAAATATTCGAAATTTGTTACCACCTCTCGGTGTCTGTTAGTATTCGCTGAGATC 327

QY 361 GCGTTTCTGGTGTAGTGTGGATATGGCCAAAACGCGCCATGTTGACTCCCTCGCTGAC 420

Db 328 GGGTTTCTGGTCTGGCTCGAT-----AAAGTCGTTTGGTTGACTGAT 378

QY 421 TTCTTCTACCGCTCTCGAGCGGTGTTGAAGTGAAGTATTTGGGGTGTGGTGGCT 480

Db 379 TTCTTCAACCGAGTCTCCGTCCTCTCCAGTCTCCACCGCGAGATCCGATCGGAAGAAG 438

QY 481 TCTGATCGGAATCTCGAATCGTATAGTCTGAGGAATGTTGGAGAGGAGGATGCTGTC 540

Db 439 ATCGGAATATTTACTATAGG---AGCTCGAGGAGTGGTTGATGAGAAAGATTCAGTT 495

QY 541 ACGTATTCGAGGGGCTTTTCCAAAGAGCCTATTTTGTCTCGAGCTGATCAGGAGTGG 600

Db 496 ACTTACTTAGAGATTTTACTAAGATCCAAATTTTATCTCTGCTGCTGAAGGACTTT 555

QY 601 AAGTCGTGTTGGTTCGATGTAAATTTGGGTTTAGTGGGGATAGAAAGCAGATCGCGCA 660

Db 556 CAATGTTGTTCTGTGGATTGTACATTTGGAGATAGTTTCAGGGGAAAACACAGATGCTGCG 615

QY 661 TTTGGGTTTACCTCAACCAAGTGAACAGCTAGCAATTCGCGATCAATGGATCAGCAGAA 720

Db 616 TTTGGATTAGGTCAGAAACCTGGAACTCTTAGTATTAATAGCTTCAGTGAATCAGACAG 675

QY 721 TACTATGCTGAGAAACAATATTGGCATGGCAAGACGGAGG---GGATATAACATCGTAAT 776

Db 676 TATTATCCAGAAATATGATCTTGACAGGCACGACGCTGGGAGAGGTTATGATATAGTAT 735

QY 777 GACAAACAGTCTATCTTCGGATGTTCTGTTGGATATTTTTCATGGGCTGAGTATGATAT 836

Db 736 GACCACTAGTCTATCATCATGATGTTCTGTTGGATATTTTTCGTTGGCGGAGTATGATAT 795

QY 837 GATGGCACCAGTGCACCGCAAAACTGAGCTCTTGACAGCTGCTTTCATTTCCCAATTG 896

Db 796 TATGTTCTCCGGTACACCAACCAAACTGAGAGAGCTATTGACAGTGTCTTATTTCTAATTG 855

QY 897 TGTGTCGAAATTTTCCGGTTTGAAGCTCTTGAGGCGCTTGAATAATCAAACTCAAAAT 956

Db 856 TGTGTCGGAATTTTTCGTTCTACAGCACTTGAGGCAATGATGATAAACTTAACATTAGAT 915

QY 957 TGAATTCCTTAGTGGTGTGTCACAGGAACCGTGTAGTGAAGAGTGAAACAAAGTGAAGCCCT 1016

Db	916	TGATTCTTATGTGGTGTGTCATCGAAACCGGATGGGAAAGTTGACAAAGTTGAAGCTCT	975	PD	06-SEP-2000.	
Qy	1017	GAAGCACTACAAATTTAGCTTAGCGTTTGAAATTCGAATCAGGAAGATTATGTAACCTGA	1076	XX	25-FEB-2000;	2000EP-00301439.
Db	976	TAAGCATACAAATTCAGTTTGGCTTTTGAGNATACTAACGAGGAAGATTATGTCACCGA	1035	XX	25-FEB-1999;	99US-0121825P.
Qy	1077	AAAAATCTTCCAATCCCTTGTGTGGAACTGTCCCTGTGGTTGTGTGCTCCAAATAT	1136	PR	05-MAR-1999;	99US-0123180P.
Db	1036	GAAGTTCTTCAATCCTTAGTTGCTGGTCCGTCCTCCCTGGTAGTTGGTCTCCAAATAT	1095	PR	09-MAR-1999;	99US-0123548P.
Qy	1137	TCAGAACTTGTCTCTCTCGGTTCATTTTACATATTAAGATAGAGAGTTGA	1196	PR	23-MAR-1999;	99US-0125788P.
Db	1096	AGAAGAAATTCGGCTCTCGGACTCATTCCTTCACATTAAGACTATGGAAGATGTAGA	1155	PR	25-MAR-1999;	99US-0126264P.
Qy	1197	GTCTGTGCAAGACCATGAGATNTCTAGCAGAAATCCGAAAGCATATATAATCAATCAT	1256	PR	29-MAR-1999;	99US-0126785P.
Db	1156	GCCAGTTGCAAGAGAAATAGATCTCGCAGCTAACCTGCTGTTATATACACACT	1215	PR	01-APR-1999;	99US-0127462P.
Qy	1257	GAGGTGGAAGTATGAGGTCCATCTGACTCTTCAAGGCCCTTGTGGATATGCGAGCTGT	1316	PR	06-APR-1999;	99US-0128234P.
Db	1216	AGATGGAATACGAGGGTCTTCAGATCTTTCAAGGCACCTTGTGATATGGCTGCTGT	1275	PR	08-APR-1999;	99US-0128714P.
Qy	1317	GCATTCAATCGTCCGCTTTTGAATTCATTGCGCCACAGTCAGTAGAGAGAAGAA	1376	PR	16-APR-1999;	99US-0128745P.
Db	1276	ACACTCTTCTGCGCTCTGCAATTTCTCTGCCACGAGGGTCCGAGAACAAAGAGAGGA	1335	PR	19-APR-1999;	99US-0130077P.
Qy	1377	TAATCCAAGCCTTAAGAGACGCTCTTCAAGT--GCACCTAGAGGGCCAGAAACCGTATA	1433	PR	21-APR-1999;	99US-0130449P.
Db	1336	AGGCCCTAATTTCAAGAAACGACCGTGCAAAATGTACGAGGGAGGATCAGACACAGTTTA	1395	PR	23-APR-1999;	99US-0130510P.
Qy	1434	TCATATCTATGTCCAGAGAAGGGGAAAGTTTGAGATGGAGTCCATTTACCTGAGGTCTAG	1493	PR	28-APR-1999;	99US-0130891P.
Db	1396	TCATGTTTTTTAGAGAAAGAGGCCGTTTGAATGGAATCAGTCTTTTGGAGGGGTAA	1455	PR	30-APR-1999;	99US-0131449P.
Qy	1494	CAATTTAATCTGAATGCTGTGAAGCTGCTGTTGTTTGAAGTTTCAAGTTCCATCCCTGAATCT	1553	PR	04-MAY-1999;	99US-0132048P.
Db	1456	AAGTGTGACTCAGGAAGCTCTAGAAATCTGCAGTTCTCGCCAACTTCAAGTCTTTAAAAACA	1515	PR	05-MAY-1999;	99US-0132407P.
Qy	1554	TGTGCTGTATGAAGCACTGAAAGGCTGAAGTATAAGAGGGGGAGTGTCTTAAAACT	1613	PR	06-MAY-1999;	99US-0132484P.
Db	1516	TGAGGCAGTGTGAAGAAAGGAAAGGCTTGAAGCTTAAAGGAGACAAAGAGCTTAAAT	1575	PR	06-MAY-1999;	99US-0132486P.
Qy	1614	CTACAAATATACCCAAATTCGCCTTGACACAGAGACAAAGCTCTTTATACCTTCAGCTTCAA	1673	PR	07-MAY-1999;	99US-0132863P.
Db	1576	ACATCGAATTTACCCGCTTGCCCTTAAGCAACGACAGGCTTTGTACAACTTCAAATTCGA	1635	PR	11-MAY-1999;	99US-0134256P.
Qy	1674	AGTGATGCTGATTCAGGAGTCACTTGGAGAACAACTCTTGTGCCAAGTTTGAAGTCAT	1733	PR	14-MAY-1999;	99US-0134218P.
Db	1636	GGGAAATTCGAGTCTAAGTAGTCACATTCACAAATTCAAACCAACCCCTTGTGCTAAATTTGAGGTGT	1695	PR	14-MAY-1999;	99US-0134219P.
Qy	1734	TTTTGTGTAG 1743		PR	14-MAY-1999;	99US-0134370P.
Db	1696	CTTCGTCTAG 1705		PR	18-MAY-1999;	99US-0134768P.
RESULT 3					PR	99US-0134768P.
ID	AAC39529 standard; DNA; 1982 BP.				PR	99US-0134941P.
XX					PR	99US-0135124P.
AC	AAC39529;				PR	99US-0135353P.
XX					PR	99US-0135629P.
DT	17-OCT-2000 (first entry)				PR	99US-0136021P.
XX	Arabidopsis thaliana DNA fragment SEQ ID NO: 24967.				PR	99US-0136392P.
DE	Hybridisation assay; genetic mapping; gene expression control;				PR	99US-0136782P.
XX	protein identification; signal transduction pathway; metabolic pathway;				PR	99US-0137222P.
KW	promoter; termination sequence; ss.				PR	99US-0137528P.
KW	Arabidopsis thaliana.				PR	99US-0137502P.
OS	EP1033405-A2.				PR	99US-0137724P.
PN					PR	99US-0138094P.
XX					PR	99US-0138540P.
					PR	99US-0138847P.
					PR	99US-0139119P.
					PR	99US-0139452P.
					PR	99US-0139457P.
					PR	99US-0139453P.
					PR	99US-0139458P.
					PR	99US-0139459P.
					PR	99US-0139460P.
					PR	99US-0139461P.
					PR	99US-0139462P.
					PR	99US-0139463P.
					PR	99US-0139750P.
					PR	99US-0139763P.
					PR	99US-0139817P.
					PR	99US-0139899P.
					PR	99US-0140353P.
					PR	99US-0140354P.
					PR	99US-0140695P.
					PR	99US-0140823P.
					PR	99US-0140991P.
					PR	99US-0141287P.
					PR	99US-0141842P.
					PR	99US-0142154P.
					PR	99US-0142055P.

PR	06-JUL-1999;	99US-0142390P.	PR	23-SEP-1999;	99US-0155486P.
PR	08-JUL-1999;	99US-0142803P.	PR	24-SEP-1999;	99US-0155659P.
PR	09-JUL-1999;	99US-0142920P.	PR	28-SEP-1999;	99US-0156458P.
PR	12-JUL-1999;	99US-0142977P.	PR	29-SEP-1999;	99US-0156596P.
PR	13-JUL-1999;	99US-0143542P.	PR	04-OCT-1999;	99US-0157117P.
PR	14-JUL-1999;	99US-0143624P.	PR	05-OCT-1999;	99US-0157753P.
PR	15-JUL-1999;	99US-0144005P.	PR	06-OCT-1999;	99US-0157865P.
PR	16-JUL-1999;	99US-0144085P.	PR	07-OCT-1999;	99US-0158029P.
PR	16-JUL-1999;	99US-0144086P.	PR	08-OCT-1999;	99US-0158232P.
PR	19-JUL-1999;	99US-0144325P.	PR	12-OCT-1999;	99US-0158369P.
PR	19-JUL-1999;	99US-0144331P.	PR	13-OCT-1999;	99US-0159293P.
PR	19-JUL-1999;	99US-0144332P.	PR	13-OCT-1999;	99US-0159294P.
PR	19-JUL-1999;	99US-0144333P.	PR	13-OCT-1999;	99US-0159295P.
PR	19-JUL-1999;	99US-0144334P.	PR	14-OCT-1999;	99US-0159329P.
PR	19-JUL-1999;	99US-0144335P.	PR	14-OCT-1999;	99US-0159330P.
PR	20-JUL-1999;	99US-0144352P.	PR	14-OCT-1999;	99US-0159331P.
PR	20-JUL-1999;	99US-0144632P.	PR	14-OCT-1999;	99US-0159637P.
PR	20-JUL-1999;	99US-0144884P.	PR	14-OCT-1999;	99US-0159638P.
PR	21-JUL-1999;	99US-0144814P.	PR	18-OCT-1999;	99US-0159584P.
PR	21-JUL-1999;	99US-0145086P.	PR	21-OCT-1999;	99US-0160741P.
PR	21-JUL-1999;	99US-0145088P.	PR	21-OCT-1999;	99US-0160767P.
PR	22-JUL-1999;	99US-0145085P.	PR	21-OCT-1999;	99US-0160768P.
PR	22-JUL-1999;	99US-0145087P.	PR	21-OCT-1999;	99US-0160770P.
PR	22-JUL-1999;	99US-0145089P.	PR	21-OCT-1999;	99US-0160814P.
PR	22-JUL-1999;	99US-0145192P.	PR	21-OCT-1999;	99US-0160815P.
PR	23-JUL-1999;	99US-0145145P.	PR	22-OCT-1999;	99US-0160980P.
PR	23-JUL-1999;	99US-0145218P.	PR	22-OCT-1999;	99US-0160981P.
PR	23-JUL-1999;	99US-0145224P.	PR	22-OCT-1999;	99US-0160989P.
PR	26-JUL-1999;	99US-0145276P.	PR	25-OCT-1999;	99US-0161404P.
PR	27-JUL-1999;	99US-0145913P.	PR	25-OCT-1999;	99US-0161405P.
PR	27-JUL-1999;	99US-0145918P.	PR	25-OCT-1999;	99US-0161406P.
PR	27-JUL-1999;	99US-0145919P.	PR	26-OCT-1999;	99US-0161359P.
PR	28-JUL-1999;	99US-0145951P.	PR	26-OCT-1999;	99US-0161360P.
PR	02-AUG-1999;	99US-0146388P.	PR	26-OCT-1999;	99US-0161361P.
PR	02-AUG-1999;	99US-0146389P.	PR	28-OCT-1999;	99US-0161920P.
PR	02-AUG-1999;	99US-0146389P.	PR	28-OCT-1999;	99US-0161922P.
PR	03-AUG-1999;	99US-0147038P.	PR	28-OCT-1999;	99US-0161933P.
PR	04-AUG-1999;	99US-0147204P.	PR	28-OCT-1999;	99US-0161933P.
PR	04-AUG-1999;	99US-0147302P.	PR	29-OCT-1999;	99US-0162142P.
PR	05-AUG-1999;	99US-0147192P.	Query Match 30.1%; Score 661.6; DB 3; Length 1982;		
PR	05-AUG-1999;	99US-0147260P.	Best Local Similarity 68.1%; Pred. No. 7.9e-166;		
PR	06-AUG-1999;	99US-0147303P.	Matches 987; Conservative 0; Mismatches 444; Indels 19; Gaps 4;		
PR	06-AUG-1999;	99US-0147416P.	Qy	301	AAGAGGAATGGAGCAATCTAATGCCCTCTTGTGTGTTCCCTTGTGGCTATCGCGAGATC 360
PR	09-AUG-1999;	99US-0147493P.	Db	267	AAGCAAAATATCGAATTTGTACCACTCTGGTGTCTCTGGTAGTTATCGCTGAGATC 326
PR	09-AUG-1999;	99US-0147935P.	Qy	361	GC GTTCTCGGTAGTTGGATATGGCCAAACGCCGCCCATGGTTGACTCCCTCGCTGAC 420
PR	10-AUG-1999;	99US-0148171P.	Db	327	GGGTTTCTGGTCTGGCTCGAT-----AAAGTCGCTTGGTTGATACGTTGACTGAT 377
PR	11-AUG-1999;	99US-0148319P.	Qy	421	TTCTTTACCGCTCTCGAGCGGTGCTTGAAGGTGACGATTTGGGTGGGTTGGTGGCT 480
PR	12-AUG-1999;	99US-0148341P.	Db	378	TTCTTACCACGATCTCGTCACTCTCCAGTCTCCACCGCGAGATCCGATCGGAAGAAG 437
PR	13-AUG-1999;	99US-0148684P.	Qy	481	TCTGATCGGAATTCGAAATCGTATAGTTGTGAGGATGTTGGAGAGGAGGATGCTGTC 540
PR	16-AUG-1999;	99US-0149368P.	Db	438	ATCGGATTTATTACTGATAGG---AGCTCGAGAGGTGGTTGATGAGAGAAGATTTCAGTT 494
PR	17-AUG-1999;	99US-0149175P.	Qy	541	ACGTATTTCGAGGGGCTTTTCCAAAGAGCCCTATTTTCTTCTGGAGCTGATCAGGAGTGG 600
PR	18-AUG-1999;	99US-0149426P.	Db	495	ACTTACTCTAGAGATTTTACTAAAGATCCAAATTTTATCTCTTGTGTGTAAGAGGACTTT 554
PR	20-AUG-1999;	99US-0149722P.	Qy	601	AAGTCGTGTTGGTGGATGTAATTTGGGTTTAGTGGGATGAAAGCAGATGCCGCA 660
PR	20-AUG-1999;	99US-0149723P.	Db	555	CAATGGTGTCTGTGGATTGTACATTTGGAGATAGTTTCAGGGAAAAACACAGATGCTGCG 614
PR	20-AUG-1999;	99US-0149923P.	Qy	661	TTTGGGTACTCTCAACCAAGTGGACAGCTAGCATTTCTGCATCAATGGATCAGCAGAA 720
PR	23-AUG-1999;	99US-0149902P.	Db	615	TTTGGATTAGTTCAGAAACCTGGAACTCTTTAGTATTAATACGTTCCATGGAAATCAGCAG 674
PR	23-AUG-1999;	99US-0149930P.	Qy	721	TACTATGCTGAGAACATATTGGCATGGCAAGACGGAGG---GGATATTAACATCGTAAT 776
PR	26-AUG-1999;	99US-0150884P.			
PR	27-AUG-1999;	99US-0151065P.			
PR	27-AUG-1999;	99US-0151066P.			
PR	27-AUG-1999;	99US-0151080P.			
PR	30-AUG-1999;	99US-0151303P.			
PR	31-AUG-1999;	99US-0151438P.			
PR	01-SEP-1999;	99US-0151930P.			
PR	07-SEP-1999;	99US-0152363P.			
PR	10-SEP-1999;	99US-0153070P.			
PR	13-SEP-1999;	99US-0153758P.			
PR	15-SEP-1999;	99US-0154018P.			
PR	16-SEP-1999;	99US-0154039P.			
PR	20-SEP-1999;	99US-0154779P.			
PR	22-SEP-1999;	99US-0155139P.			

301 AAGAGGAAATGGAGCAATCTAATGCCCTCTTGTGTTGTTGCCCTTGTGGTCATCGCGGAGATC 360

Db 166 AGCGGGCGCTGGGGTGTCTCTCTGCGCTCTCTGCTGGCGCGCGCTCTCTCGCGGAGATC 225  
 QY 361 GCGTTTCTGGGTAGTGTGATATGCGCAAAACGCGCCATGTTGACTCCCTCGCTGAC 420  
 Db 226 GCGTTCTCGCGCCCTCGACATGCGCAAGAAAGCGCGGCTCGAGAGCTGGACACC 285  
 QY 421 TTCTTCTACCGCTCTCGAGCGGTGTTTGAAGGTGACGATTTGGGGTGTGGGTGCTGGCT 480  
 Db 286 TCCTTTTACCGCGCTCTCGCGGATTTGGCGGATGCGGTTGGCGGGCGCGAGCTCGAGG 345  
 QY 481 TCTGATCGGAATTTCTGAATCGTATAGT-----TGTGAGAAATGGTTGGAGAGGAG 531  
 Db 346 GCAGGCGCGACAGCGAGGACGAAGAGATCCGGCTGTGCGAGCAGCGCTCGAGAGGGAG 405  
 QY 532 GATGCTGTACGATTTCTGAGGGGCTTTTCCAAAGAGCCTATTTTGTCTGCGAGCTGAT 591  
 Db 406 GATGCGGTGCGCTACGACCGGACTTTGACAGTGATCCCGTGTGCTGGTGGCGCTGCC 465  
 QY 592 CAGGAGTGGAGTGTGTTCCGTTTGGATGTAAATTTGGGTTTGTAGTGGGATAGAAAGCCA 651  
 Db 466 AAGGATTGGAATAAATCTACGTAGGATGTGAATTTGGTTTCTCGAGTAAGACACCT 525  
 QY 652 GATGCCCGATTTGGGTACCTCAACCAAGTGGACAGCTAGCATTTGCGCATCAATGGAA 711  
 Db 526 GATGCTACATTTGGAATTTGACACAGATCTCTGTAGATGCTATCTCTCAGATCAATGGAA 585  
 QY 712 TCAGCAGAACTACTGCTGAGAACATATTCATGCGCAAGAGCGGAGGATATACATC 771  
 Db 586 TCATCTCAATATTTTACAGAGAATAATTTGATGTGGCTCGAGGAGAGGATACAGATT 645  
 QY 772 GTAATGACAAACAGCTCTATCTTCGGATGTTTCTGTTGGATATTTTTCATGGGCTGAGTAT 831  
 Db 646 GTGATGACAAACAGCTCTTCTTACAGGTACAGTTGGCTACTTTTTCATGGGCTGATAT 705  
 QY 832 GATAATGATGCAACAGTGCAGCGCGAAATGAAAGTGTCTTTCAGAGCTGTTTCATTTC 891  
 Db 706 GATATCATGCACTGTGCTTCCAAAGATGAAAGAGCTCTTGTGCGAGCTTTATTCT 765  
 QY 892 AATTTGGTCTCGAAATTTCCGGTTGCAAGCTCTTGGAGCCCTTGAANAATCAACATC 951  
 Db 766 AACTGTGGTGCAGAACTTTCTGTTGCAAGCCCTTGAGATGCTTGAAACTTTGGATGTC 825  
 QY 952 AAAATTTGATTTCTATGTTGTTGTTGTCAGGAAACGTTGATGGAAGAGTGAACAAGTGGAA 1011  
 Db 826 AAAATGATTTCTATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 885  
 QY 1012 GCCTGAGACATCAAAATTTAGCTTAGCTTTGAAATTTGAAATTTGAAATTTGAAATTTGAA 1071  
 Db 886 ACTTTGAAAGGCTACAGATTCAGCTTGGCATTTTGAGAAATTTCTAATGAGGAGGATTATGA 945  
 QY 1072 ACTGAAATTTCTTCAATCCCTTGTGCTGGAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1131  
 Db 946 ACTGAAATTTTCTTCACTAGTACAGGTTCTTATTCGGTGTGTTGTTGTTGTTGTTGTTGTT 1005  
 QY 1132 AATATTGAGACTTTGCTCTCTCTCTGTTTCAATTTTACATATTAAAGAGATAGAGGAT 1191  
 Db 1006 AATATTCAAGATTTTCTCGGAGAGAGGCGCAATATTACATATTAAAGAGCTTGATAT 1065  
 QY 1192 GTTGAGTCTGTTGCAAGACCATGAGATATCTAGCAGAAATCCCGAAGCATATATCAA 1251  
 Db 1066 GTTGCTTCACTGTTGCAAGCAATGAAATATTGCTTCAACCTGATGCTTCAATCAA 1125  
 QY 1252 TCATTGAGTGGAGATAGGTTCCATCTGACTCTTCAAGCCCTTGTGGATATGGCA 1311  
 Db 1126 TCTTTGAGTGGAGATATGATGTTCCATCCGATTTCTTTCAAGCTCTTATTTGATCATGGCA 1185  
 QY 1312 GCTGTGCTATTCATGCTGCGCTTCTTGCATTTCACTTGGCCACAGTGTAGTAGAGAGGAA 1371  
 Db 1186 GCGGTTCAATCTCTTGTGCTCTTTGTATACATATTGCTACCAAGATTCATTTAAAGGAG 1245  
 QY 1372 GAAATTAATCCAGCCCTTAAGACGCTCTTGAAGTGCATAGAGGGCGCAGAAACCGTA 1431  
 Db 1246 GAAAGGACTCCAAATTTTACAAATCGTCTTGTAGCTGTTTCCACCAAAAGGGAACAAT 1305

QY 1432 TATCATATCTATGCTCAGAGAAAGGGGAGGTTTGAGATGAGTCCATTTTACCTGAGGTCT 1491  
 Db 1306 TACCACCTTATTTATCCGAGAGAGAGGCGGTTTAACTCAGAGAGCATTTTACATGATCA 1365  
 QY 1492 AGCAATTTAACTCTGAATGCTGTGAAGGCTGCTGTTGTTTGAAGTTCAATCCCTGAAT 1551  
 Db 1366 GGGCAGTTAACTCTGGAGGCTTGGAAATCCGAGTGTCCGTAATTTAGGTCCTCAAC 1425  
 QY 1552 CTGTGCTCTATGAGAGACTGAAAGGCTGAAGTTTAAAGAGGGGAGTGTCTTTAA 1611  
 Db 1426 CAGGTTCTGTATGGAAGGATGAAAGGCCACCGAGCATTTAGAGTGGGATGACCTGAA 1485  
 QY 1612 CTCTACAAATATACCAATTTGCTTGACACAGAGCAAGCTCTTTATACCTTTCACTTC 1671  
 Db 1486 TTATACAGATTTTACCAGTCCGTCTAACGCAACGTCAGCTTTGTACGTTTATGATTT 1545  
 QY 1672 AAAGGTGATGCTGATTTTCAAGGAGTCACTTTGGAGAAACAATCTTTGTCCTCAAGTTGAATC 1731  
 Db 1546 AGGGATGATTTCTGAACTCGAGCAATATATCAAAAGACCATCCCTGTGCAAAAGCTTGAAGTA 1605  
 QY 1732 ATTTTGTGTAGC 1744  
 Db 1606 ATTTTGTGTAAAC 1618

RESULT 5

ACN54249  
 ID ACN54249 standard; cDNA; 650 BP.  
 XX ACN54249;  
 XX AC  
 DT 02-DEC-2004 (first entry)  
 XX DE  
 DE Cotton androecium tissue EST Clone ID: LIB3828-022-Q1-K6-F4, SEQ:9030.  
 XX KW  
 KW Cotton; plant; EST; expressed sequence tag; transgenic plant; androecium;  
 KW variety Nucotton33B; library LIB3828; molecular tag; molecular marker;  
 KW genetic mapping; molecular mapping; seed germination; plant growth;  
 KW plant quality; plant yield; plant breeding; tissue printing; ss.  
 XX OS  
 OS Gossypium hirsutum.  
 XX PN  
 PN US2004123340-A1.  
 XX XX  
 PD 24-JUN-2004.  
 XX PF  
 PF 12-DEC-2001; 2001US-00021323.  
 XX PR  
 PR 14-DEC-2000; 2000US-0255619P.  
 XX PA  
 PA (DEIK/) DEIKMAN J.  
 PA (FENG/) FENG P C C.  
 PA (FINC/) FINCHER K L.  
 PA (ZIEG/) ZIEGLER T E.  
 PI Deikman J, Feng PCC, Fincher KL, Ziegler TE;  
 XX WPI; 2004-479808/45.  
 XX DR  
 DR New isolated nucleic acid molecule that encodes a plant protein or its  
 PT fragment, useful for isolating a variety of agronomically significant  
 PT genes associated with plant growth, quality or yield, and as molecular  
 PT tags to map genes.  
 XX PS  
 PS Claim 1; SEQ ID NO 9030; 34pp; English.  
 XX CC  
 CC The invention relates to 17880 cotton expressed sequence tags (ESTs;  
 CC ACN45220-ACN63099). The ESTs were isolated from cDNA libraries generated  
 CC from primed or non-primed seeds from variety DP50B, mature seeds from  
 CC variety Coker 312 Boswell 96 Field, and androecium tissue, gynoeium  
 CC tissue, developing fibres, carpel walls and septa from variety  
 CC Nucotton33B. The invention also relates to substantially purified

CC proteins or their fragments encoded by nucleic acid molecules of the  
CC invention, and to transformed plants having a nucleic acid construct  
CC comprising a nucleic acid of the invention. The cotton ESTs are useful as  
CC molecular tags to isolate genetic regions, to isolate genes, to map  
CC genes, to determine gene function and to determine whether genes are  
CC members of a particular gene family. The nucleic acid molecules may be  
CC used for isolating a variety of agronomically significant genes  
CC associated with plant growth, quality, yield, and could also serve as  
CC links in metabolic and catabolic pathways. The nucleic acid molecules are  
CC also useful for identifying genes important in initiating and maintaining  
CC seed germination or that may be used to mitigate stresses encountered  
CC during seed germination. The ESTs additionally enable the acquisition of  
CC promoters and cis-regulatory elements which will be useful to express  
CC agronomically significant genes in these tissues and/or other tissues,  
CC and also permits the acquisition of molecular markers useful in breeding  
CC schemes, genetic and molecular mapping, and in cloning of agronomically  
CC significant genes. The nucleic acid molecules are further useful for  
CC detecting the expression level or pattern of a protein or mRNA and for  
CC present sequence represents a specifically claimed EST isolated from a  
CC cotton variety Nucleon33B androecium tissue cDNA library (LIB3828). The  
CC sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from the US  
CC patent office at seqdata.uspto.gov/sequence.html?DocID=US20040123340  
XX  
SQ Sequence 650 BP; 181 A; 135 C; 160 G; 173 T; 0 U; 1 Other;

Query Match 11.2%; Score 245.2; DB 13; Length 650;  
Best Local Similarity 71.5%; Pred. No. 9.4e-55;  
Matches 336; Conservative 0; Mismatches 133; Indels 1; Gaps 1;

QY 1273 GGTTCATCTGATCTCTTCAAGCCCTTGGATATGGAGCTGTCATTCATCGTCCGT 1332  
DB 34 GGGCCGACCGATACITTCAGGCTCTTCGATATGGCTGCGGTTCATTCGTCATCGGT 93  
QY 1333 CTTTGCATTCACATGAGTACAGTACAGTACAGTACAGTACAGTACAGTACAGTACAGT 1392  
DB 94 TTGTGCATTCACATGAGTACAGTACAGTACAGTACAGTACAGTACAGTACAGTACAGT 152  
QY 1393 AGAGCTCTGTCAGTACAGTACAGTACAGTACAGTACAGTACAGTACAGTACAGTACAGT 1452  
DB 153 AAACGTCCTCGCAAGTACAGTACAGTACAGTACAGTACAGTACAGTACAGTACAGTACAGT 212  
QY 1453 AGGGAAGGTTTGAGATGGAGTCCATTTACCTGAGTCTAGCAATTTAACTCTGATGCT 1512  
DB 213 CGAGGAGGTTTGAGATGGAGTCCATTTTCTTAAGGTCCGGAATATGACCTTAAAGGCC 272  
QY 1513 GTGAAGCTGCTGTTGTTTGAAGTTCACATCCCTGAATCTTGTGCTGTATGGAAGACT 1572  
DB 273 TTGAGGCTGCGGTTTACAGGCTTTCAAGTTCGGAACACGTTCTTATTTGGAACCG 332  
QY 1573 GAAAGGCTGAGTTTAAAGAGGGGGGAGTGTCTTTAAACTCTACAAATATATACCAAT 1632  
DB 333 GAAAGGCGAAGAACCTTCGAGGTGGAGATGAATGAATGAATGAATGAATGAATGAATGAAT 392  
QY 1633 GGCTTGACACAGACAGAGCTCTTTTATACCTTCAGTCTTAAAGTGTATGCTGATTTGAG 1692  
DB 393 GGGTTGACACAAAGACAGGCTTTATATACATTTCAAGTTTCAAGGGGATGCTGATCTTAAG 452  
QY 1693 AGTCATTTGGAGAACATCTTGTGCGCAAGTTTGAAGTCAATTTTGTGTA 1742  
DB 453 AACCATATCGAAGAACACCTTTGCGGAAGTTCGAAGTCATATTCGIGTA 502

RESULT 6  
AAF84907  
ID AAF84907 standard; DNA; 2069 BP.

XX AAF84907;  
AC  
XX Nitrogen-inducible promoter for regulating foreign gene expression.  
DT 09-JUL-2001 (first entry)  
DE

XX nitrogen-inducible promoter; nitrite reductase gene; NiR gene;  
KW transgenic plant; transgene expression; ss.  
XX Synthetic.  
OS  
XX WO200125454-A2.  
PN  
XX 12-APR-2001.  
PD  
XX 02-OCT-2000; 2000WO-CA001143.  
PF  
XX 04-OCT-1999; 99US-0157133P.  
PR  
XX (MEDI-) MEDICAGO INC.  
PA  
XX Vezina L, D'aoust M;  
PI  
XX WPI; 2001-308228/32.  
DR  
XX Regulating foreign gene transcription in transgenic plants, comprises  
PT transforming a plant (cell) with an expression construct having nitrogen-  
PT inducible promoter, an open reading frame of a gene and a polyadenylation  
PT site.  
PT  
PS Claim 1; Page 30-31; 44pp; English.  
XX  
XX AAF84905-17 represent nitrogen-inducible promoters. They are promoters of  
CC the nitrite reductase (NiR) gene. The promoter is used for regulating  
CC foreign gene transcription in transgenic organisms. The method uses an  
CC expression construct having a nitrogen-inducible promoter, with(out) cis-  
CC acting sequence, operably linked to the gene to be expressed and  
CC modulated for transcriptional expression of the gene by addition or  
CC removal of a nitrogen inducer, an open reading frame of a gene, and a 3'  
CC polyadenylation signal. The method is useful for regulating the  
CC transcription of transgenes in genetically modified organisms. The  
CC nitrogen-inducible expression cassettes are useful for the controlling  
CC expression of foreign genes in plants  
XX  
SQ Sequence 2069 BP; 640 A; 389 C; 335 G; 705 T; 0 U; 0 Other;

Query Match 9.5%; Score 209.4; DB 4; Length 2069;  
Best Local Similarity 66.5%; Pred. No. 6e-45;  
Matches 341; Conservative 0; Mismatches 151; Indels 21; Gaps 2;

QY 1486 AGGCTAGCAATTTAACTCTGAAGCTGTGAAGGCTGCTGTTTGAAGTTACATCC 1545  
DB 170 AGATCTAGCAATTTAACTCTGAAGCTGTGAAGGCTGCTGTTTGAAGTTACATCC 229  
QY 1546 CTGAATCTTGTGCTGTATGGAAGCTGAAAGGCTGAAAGTATATAAGAGGGGGAGTGTCT 1605  
DB 230 CTGAATCTATGTTTCTGTATGGAAGCTGAAAGGCTGAAAGTATATAAGAGGGGGAGTGTCT 289  
QY 1606 TTAAACTCTACAAATATACCAATTTGGCTTTGACACAGAGCAAGCTCTTTATACCTTC 1665  
DB 290 TTGAAGGTTTACAAATATATACCTTCGGGCTTTGACACAGAGCAAGCTCTTTATACCTTC 349  
QY 1666 AGCTTCAAAGGTTGATCTGATTTTCAAGAGTCACTTGGAGAGCAATCTTGTGCGAAGTTT 1725  
DB 350 CAGTTCAAAGGAGTGTGATTTTCAAGAGTCACTTGGAGAGCAATCTTGTGCGAAGTTT 409  
QY 1726 GAAGTCAATTTTGTGTAGCATGCGCTAA -----ATGGTACCTCTGCTTACCTGAAT 1778  
DB 410 GAAGTAAATTTTGTGTAGCATGATGTTGAGTCACTTACATTTACATGATCACCTAGCAT 469  
QY 1779 AGCTTCACTTAGCTGAGCACTAGCTAGAGTTTTAGGAATGAGTATGCGATGATATGCG 1838  
DB 470 AGCTCTTTCACTTAAGTACGAGATGAAGTTTTAGGAATGAGTATGAGTATGAGTATGCG 529  
QY 1839 ATGGCTT-----TATTTATGCTTGTGTTTCTTGGCAACTCATTTGATGTTT 1884  
DB 530 ATGGCTTGTGAATGCTTACCTTACTTTGGCCAACTCATCGGGGATTTACATTTCAAGAA 589





CC	expression of foreign genes in plants	
XX		
SQ	Sequence 2165 BP; 664 A; 424 C; 345 G; 732 T; 0 U; 0 Other;	
	Query Match 9.5%; Score 209.4; DB 4; Length 2165;	
	Best Local Similarity 66.5%; Pred. No. 6.1e-45;	
	Matches 341; Conservative 0; Mismatches 151; Indels 21; Gaps 2;	
QY	1486 AGGCTCTAGCAATTTAACTCTGAATGCTGTGAAGGCTGCTGTGTTTGAAGTTCAATCC 1545	
DB		
	170 AGATCTAGCAATTTAACTCTGGAGTCTTCAAGACTGCTGTCTTACGAAGTTCAGCTCC 229	
QY	1546 CTGAATCTTTGTGCTGTATGGAAGACTGAAAGCCCTGAAAGTTTATAAGAGGGGGAAGTCT 1605	
DB		
	230 CTGAATCATGTTCTGTATGGAAGCCCTGAAAGACCTCAAAATCTTAAAGGTGGCGATAAA 289	
QY	1606 TTAATACTTACAAAATATACCAATTTGGCTTGACACAGACAGCAAGCTCTTTATACCTTC 1665	
DB		
	290 TTGAAGGTTTACAAAATATACCCCTGGCGCTTGACACAGAGGCAAGCTCTTTATACCTTC 349	
QY	1666 AGCTTCAAAAGTGTAGTCTGAAAGTCTGAAAGCCCTGAAAGTTTATAAGAGGGGGAAGTCT 1725	
DB		
	1726 GAAAGTCAATTTTGTAGCATGCGCTAA-----ATGGTACCTCTGCTCACTCAATTT 1778	
DB		
	410 GAAGTAAATTTTGTGTAGCATATGTTGAGCTACCTACAATTTACATGATCACCTAGCATTT 469	
QY	1779 AGCTTCACTTAGCTAGACACTAGTAGAGTTTTAGGAATGAGTATGGCAGTGAATATGGC 1838	
DB		
	470 AGCTTCTTCACTTAACTGAGAGAAATGAAGTTTTAGGAATGAGTATGACCATGGAGTCGGC 529	
QY	1839 ATGGCTT-----TATTTATGCTAGTTCTTGGCCAACTCATCTGCTACTGATGTTT 1884	
DB		
	530 ATGGCTTTGTAATGCCCTACCTACTTTGGCCAACTCATCGGGATTTACATTCAGAAAT 589	
QY	1885 GTATAAGACATCACACTTTAACTTTTAACTTTGTTCTGTAGAAGTGCAAATCCATATTTA 1944	
DB		
	590 ATACATGACTTCAACCATACCTTAAACCCCTTTTGTAGAATACTGAATGTTTCATATTTA 649	
QY	1945 ATGCTTAGTTTATAGTCTCTTATCTGATCATCT 1977	
DB		
	650 ATGTTGGGTTGTAGTGTGTTTTTACTTGTATATAT 682	
	RESULT 9	
AAF84916	AAF84916 standard; DNA; 2232 BP.	
AC	AAF84916;	
AC	AC	
XX	09-JUL-2001 (first entry)	
DT	09-JUL-2001 (first entry)	
DE	Nitrogen-inducible promoter for regulating foreign gene expression.	
XX		
XX	nitrogen-inducible promoter; nitrite reductase gene; NiR gene;	
KW	transgenic plant; transgene expression; ss.	
XX		
OS	Synthetic.	
XX		
PN	WO200125454-A2.	
XX		
PD	12-APR-2001.	
XX		
PP	02-OCT-2000; 2000WO-CA001143.	
XX		
PR	04-OCT-1999; 99US-0157133P.	
XX		
PA	(MEDI-) MEDICAGO INC.	
XX		
PI	Vezina L, D'aout M;	
XX		
DR	WPI; 2001-308228/32.	

XX	Regulating foreign gene transcription in transgenic plants, comprises
PT	transforming a plant (cell) with an expression construct having nitrogen-
PT	inducible promoter, an open reading frame of a gene and a polyadenylation
PT	site.
XX	
XX	Claim 1; Page 37-38; 44pp; English.
XX	
CC	AAF84905-17 represent nitrogen-inducible promoters. They are promoters of
CC	the nitrite reductase (NiR) gene. The promoter is used for regulating
CC	foreign gene transcription in transgenic organisms. The method uses an
CC	expression construct having a nitrogen-inducible promoter, with(out) cis-
CC	acting sequence, operably linked to the gene to be expressed and
CC	modulated for transcriptional expression of the gene by addition or
CC	removal of a nitrogen inducer, an open reading frame of a gene, and a 3'
CC	polyadenylation signal. The method is useful for regulating the
CC	transcription of transgenes in genetically modified organisms. The
CC	nitrogen-inducible expression cassettes are useful for the controlling
CC	expression of foreign genes in plants
XX	
SQ	Sequence 2232 BP; 686 A; 436 C; 362 G; 748 T; 0 U; 0 Other;
	Query Match 9.5%; Score 209.4; DB 4; Length 2232;
	Best Local Similarity 66.5%; Pred. No. 6.2e-45;
	Matches 341; Conservative 0; Mismatches 151; Indels 21; Gaps 2;
QY	1486 AGGCTCTAGCAATTTAACTCTGAATGCTGTGAAGGCTGCTGTGTTTGAAGTTCAATCC 1545
DB	
	170 AGATCTAGCAATTTAACTCTGGAGTCTTCAAGACTGCTGTCTTACGAAGTTCAGCTCC 229
QY	1546 CTGAATCTTTGTGCTGTATGGAAGACTGAAAGCCCTGAAAGTTTATAAGAGGGGGAAGTCT 1605
DB	
	230 CTGAATCATGTTCTGTATGGAAGCCCTGAAAGACCTCAAAATTTCTAAAAGGTGGCGATAA 289
QY	1606 TTAATACTTACAAAATATACCAATTTGGCTTGACACAGACAGCAAGCTCTTTATACCTTC 1665
DB	
	290 TTGAAGGTTTACAAAATATACCCCTGGCGCTTGACACAGAGGCAAGCTCTTTATACCTTC 349
QY	1666 AGCTTCAAAAGTGTAGTCTGAAAGTCTGAAAGCCCTGAAAGTTTATAAGAGGGGGAAGTCT 1725
DB	
	350 CAGTTCAACGGGATGTTGATTTTCAAGAGTCACTTGGAGAGCAATCTTGTGCCAAGTTT 409
QY	1726 GAAGTCAATTTTGTGTAGCATGCGCTAA-----ATGGTACCTCTGCTCACTCAATTT 1778
DB	
	410 GAAGTAAATTTTGTGTAGCATATGTTGAGCTACCTACAATTTACATGATCACCTAGCATTT 469
QY	1779 AGCTTCACTTAGCTAGACACTAGTAGAGTTTTAGGAATGAGTATGGCAGTGAATATGGC 1838
DB	
	470 AGCTTCTTCACTTAACTGAGAGAAATGAAGTTTTAGGAATGAGTATGACCATGGAGTCGGC 529
QY	1839 ATGGCTT-----TATTTATGCTAGTTCTTGGCCAACTCATCTGCTACTGATGTTT 1884
DB	
	530 ATGGCTTTGTAATGCCCTACCTACTTTGGCCAACTCATCGGGATTTACATTCAGAAAT 589
QY	1885 GTATAAGACATCACACTTTAACTTTTAACTTTGTTCTGTAGAAGTGCAAATCCATATTTA 1944
DB	
	590 ATACATGACTTCAACCATACCTTAAACCCCTTTTGTAGAATACTGAATGTTTCATATTTA 649
QY	1945 ATGCTTAGTTTATAGTCTCTTATCTGATCATCT 1977
DB	
	650 ATGTTGGGTTGTAGTGTGTTTTTACTTGTATATAT 682
	RESULT 10
AAF84906	AAF84906 standard; DNA; 2808 BP.
ID	AAF84906
XX	
XX	09-JUL-2001 (first entry)
DT	09-JUL-2001 (first entry)
DE	Nitrogen-inducible promoter for regulating foreign gene expression.
XX	
XX	nitrogen-inducible promoter; nitrite reductase gene expression.
KW	
XX	
OS	
XX	
PN	
XX	
PD	
XX	
PP	
XX	
PR	
XX	
PA	
XX	
PI	
XX	
DR	

KW nitrogen-inducible promoter; nitrite reductase gene; NiR gene;  
 KW transgenic plant; transgene expression; ss.  
 OS Synthetic.  
 XX WO200125454-A2.  
 XX 12-APR-2001.  
 XX 02-OCT-2000; 2000WO-CA001143.  
 XX 04-OCT-1999; 99US-0157133P.  
 XX (MEDI-) MEDICAGO INC.  
 XX Vezina L, D'aoust M;  
 XX WPI; 2001-308228/32.  
 XX Regulating foreign gene transcription in transgenic plants, comprises  
 PT transforming a plant (cell) with an expression construct having nitrogen-  
 PT inducible promoter, an open reading frame of a gene and a polyadenylation  
 PT site.  
 XX Claim 1; Page 29-30; 44pp; English.  
 XX AAF84905-17 represent nitrogen-inducible promoters. They are promoters of  
 CC the nitrite reductase (NiR) gene. The promoter is used for regulating  
 CC foreign gene transcription in transgenic organisms. The method uses an  
 CC expression construct having a nitrogen-inducible promoter, with(out) cis-  
 CC acting sequence, operably linked to the gene to be expressed and  
 CC modulated for transcriptional expression of the gene by addition or  
 CC removal of a nitrogen inducer, an open reading frame of a gene, and a 3'  
 CC polyadenylation signal. The method is useful for regulating the  
 CC transcription of transgenes in genetically modified organisms. The  
 CC nitrogen-inducible expression cassettes are useful for the controlling  
 CC expression of foreign genes in plants  
 XX Sequence 2808 BP; 879 A; 502 C; 481 G; 946 T; 0 U; 0 Other;  
 SQ Query Match 9.5%; Score 209.4; DB 4; Length 2808;  
 Best Local Similarity 66.5%; Pred. No. 6.9e-45;  
 Matches 341; Conservative 0; Mismatches 151; Indels 21; Gaps 2;  
 QY 1486 AGGCTAGCAATTTAACTCTGAATCTGTGAAGGCTGCTGTGTTTGAAGTTTCATCTC 1545  
 DB 909 AGATCTAGCAATTTAACTCTGAATCTGTGAAGGCTGCTGTGTTTGAAGTTTCATCTC 968  
 QY 1546 CTGAATCTGTGCTGTATGGAAGCTGAAAGGCTGCTGTGTTTGAAGTTTCATCTC 1605  
 DB 969 CTGAATCTGTGCTGTATGGAAGCTGAAAGGCTGCTGTGTTTGAAGTTTCATCTC 1028  
 QY 1606 TTAAGCACTCTCAAAATATACCCAAATGCGTGTGACAGACAGCAAGCTCTTTATACCTTC 1665  
 DB 1029 TTGAAGGTTTACAAATATACCCCTCGGGCTTGACAGAGGCAAGCTCTTTATACCTTC 1088  
 QY 1666 AGCTTCAAGGTTGATGCTGATTTTCAAGGCTGCTGTGGAAGCAATCTTGTGCGCAAGTTT 1725  
 DB 1089 CAGTTTCAACGGGATGTTGATTTTCAAGGCTGCTGTGGAAGCAATCTTGTGCGCAAGTTT 1148  
 QY 1726 GAAGTCATTTTGTGTAGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1778  
 DB 1149 GAAGTCATTTTGTGTAGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1208  
 QY 1779 AGCTTCACTTAGCTAGCACTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCT 1838  
 DB 1209 AGCTTCACTTAGCTAGCACTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCT 1268  
 QY 1839 ATGGCTT-----TATTATGCTTAGTTTCTTGGCCAACTCAITTAGTGTGTTT 1884  
 DB 1269 ATGGCTTGTATGCTTACCTTACTTTGGCCAACTCAITTAGTGTGTTTCAITTCAGAAAAT 1328  
 QY 1885 GTATAAGCATCACACTTTAACTTTTAACTTTGTTCTGTAGAGTGCAATCCATATTTA 1944

DB 1329 ATACATGACTTCAACCATACCTTAAACCCCTTTTGTGAAGATAACTGAATGTTTATATTA 1388  
 QY 1945 ATGCTTAGTTTGTAGTCTCTTAATCTGATCATCT 1977  
 DB 1389 ATGTTGGTGTGTAGTGTGTTTACTTGATATAT 1421  
 RESULT 11  
 AAF84909  
 ID AAF84909 standard; DNA; 2863 BP.  
 XX AAF84909;  
 XX 09-JUL-2001 (first entry)  
 XX Nitrogen-inducible promoter for regulating foreign gene expression.  
 DE nitrogen-inducible promoter; nitrite reductase gene; NiR gene;  
 KW transgenic plant; transgene expression; ss.  
 XX Synthetic.  
 XX WO200125454-A2.  
 XX 12-APR-2001.  
 XX 02-OCT-2000; 2000WO-CA001143.  
 XX 04-OCT-1999; 99US-0157133P.  
 XX (MEDI-) MEDICAGO INC.  
 XX Vezina L, D'aoust M;  
 XX WPI; 2001-308228/32.  
 XX Regulating foreign gene transcription in transgenic plants, comprises  
 PT transforming a plant (cell) with an expression construct having nitrogen-  
 PT inducible promoter, an open reading frame of a gene and a polyadenylation  
 PT site.  
 XX Claim 1; Page 31-32; 44pp; English.  
 XX AAF84905-17 represent nitrogen-inducible promoters. They are promoters of  
 CC the nitrite reductase (NiR) gene. The promoter is used for regulating  
 CC foreign gene transcription in transgenic organisms. The method uses an  
 CC expression construct having a nitrogen-inducible promoter, with(out) cis-  
 CC acting sequence, operably linked to the gene to be expressed and  
 CC modulated for transcriptional expression of the gene by addition or  
 CC removal of a nitrogen inducer, an open reading frame of a gene, and a 3'  
 CC polyadenylation signal. The method is useful for regulating the  
 CC transcription of transgenes in genetically modified organisms. The  
 CC nitrogen-inducible expression cassettes are useful for the controlling  
 CC expression of foreign genes in plants  
 XX Sequence 2863 BP; 890 A; 525 C; 485 G; 963 T; 0 U; 0 Other;  
 SQ Query Match 9.5%; Score 209.4; DB 4; Length 2863;  
 Best Local Similarity 66.5%; Pred. No. 7e-45;  
 Matches 341; Conservative 0; Mismatches 151; Indels 21; Gaps 2;  
 QY 1486 AGGCTAGCAATTTAACTCTGAATCTGTGAAGGCTGCTGTGTTTGAAGTTTCATCTC 1545  
 DB 909 AGATCTAGCAATTTAACTCTGAATCTGTGAAGGCTGCTGTGTTTGAAGTTTCATCTC 968  
 QY 1546 CTGAATCTGTGCTGTATGGAAGCTGAAAGGCTGCTGTGTTTGAAGTTTCATCTC 1605  
 DB 969 CTGAATCTGTGCTGTATGGAAGCTGAAAGGCTGCTGTGTTTGAAGTTTCATCTC 1028  
 QY 1606 TTAAGCACTCTCAAAATATACCCAAATGCGTGTGACAGACAGCAAGCTCTTTATACCTTC 1665  
 DB 1029 TTGAAGGTTTACAAATATACCCCTCGGGCTTGACAGAGGCAAGCTCTTTATACCTTC 1088



PT Regulating foreign gene transcription in transgenic plants, comprises  
 PT transforming a plant (cell) with an expression construct having nitrogen-  
 PT inducible promoter, an open reading frame of a gene and a polyadenylation  
 PT site.

XX Claim 1; Page 36-37; 44pp; English.

XX AAF84905-17 represent nitrogen-inducible promoters. They are promoters of  
 CC the nitrite reductase (Nir) gene. The promoter is used for regulating  
 CC foreign gene transcription in transgenic organisms. The method uses an  
 CC expression construct having a nitrogen-inducible promoter, with(out) cis-  
 CC acting sequence, operably linked to the gene to be expressed and  
 CC modulated for transcriptional expression of the gene by addition or  
 CC removal of a nitrogen inducer, an open reading frame of a gene, and a 3'  
 CC polyadenylation signal. The method is useful for regulating the  
 CC transcription of transgenes in genetically modified organisms. The  
 CC nitrogen-inducible expression cassettes are useful for the controlling  
 CC expression of foreign genes in plants

XX Sequence 2971 BP; 925 A; 549 C; 508 G; 989 T; 0 U; 0 Other;

Query Match 9.5%; Score 209.4; DB 4; Length 2971;

Best Local Similarity 66.5%; Pred. No. 7.1e-45;

Matches 341; Conservative 0; Mismatches 151; Indels 21; Gaps 2;

Qy	1486	AGGCTAGCAATTTAACTCTGAATGCTGTGAAGGCTGCTGTGTTTGAAGTTCACATCC	1545
Db	909	AGATCTAGCAATTTAACTCTGAAGGCTGTGTTTGAAGTTCACATCC	968
Qy	1546	CTGAATCTGTGCTGTATGAAGCTGAAGGCTGAAGTATAAGAGGGGGAGTCT	1605
Db	969	CTGAATCATGTTCTGTATGAAGCTGAAGGCTGAAGTATAAGAGGGGGAGTCT	1028
Qy	1606	TTAAACTCTCAAAATATACCAATGCTGTGACAGACAGACAGCTCTTTATACCTTC	1665
Db	1029	TTGAAGGTTTACAAATATACCTGCGGCTTGACAGAGGCAAGCTCTTTATACCTTC	1088
Qy	1666	AGCTTCAAGTGTGCTGTATGAAGCTGAAGGCTGAAGTATAAGAGGGGGAGTCT	1725
Db	1089	CAGTTCACAGGGGATGTTGATTTTCAAGTCACTTTGAGAGCAATCTTTATACCTTC	1148
Qy	1726	GAAGTCAATTTTGTGTAGCATGCGCTAA-----ATGGTACCTCTGCTACCTGAAT	1778
Db	1149	GAAGTAAATTTTGTGTAGCATGTTGAGTACCTTACATGATCATCAGTACAT	1208
Qy	1779	AGCTTCACTTACCTAGCAGCACTAGTATGAGTATGAGTATGAGTATGAGTATGAGT	1838
Db	1209	AGCTCTTTTCACTTAACTAGAGCAATGAAGTATGAGTATGAGTATGAGTATGAGT	1268
Qy	1839	ATGGCTT-----TATTTATGCTAGTCTTCTGGCCAACTCATTTGATGTTT	1884
Db	1269	ATGGCTTGTGATGCTACCTTCTGGCCAACTCATCGGGGATTTACATTCAGAAAT	1328
Qy	1885	GTATAAGACATCACACTTTAAATTTTAACTTGTCTGTAGAAGTGCATATTTA	1944
Db	1329	ATACATGACTTCAACCACTTAAACCCCTTTTGTAGATCACTGAATGTTTATTTA	1388
Qy	1945	ATGCTTGTAGTCTTATCTGATCATCT 1977	
Db	1389	ATGTTGGGTGTAGTCTTATCTGATCATCT 1421	

RESULT 14

ID AAF84905 standard; DNA; 3714 BP.

XX AAF84905;

XX 23-JUL-2001 (first entry)

DE Nitrogen-inducible promoter for regulating foreign gene expression.

XX nitrogen-inducible promoter; nitrite reductase gene; Nir gene;

KW transgenic plant; transgene expression; ss.  
 XX Synthetic.  
 OS WO200125454-A2.  
 XX 12-APR-2001.  
 XX 02-OCT-2000; 2000WO-CA001143.  
 XX 04-OCT-1999; 99US-0157133P.  
 XX (MEDI-) MEDICAGO INC.  
 XX Vezina L, D'aoust M;  
 XX WPI; 2001-308228/32.  
 XX Regulating foreign gene transcription in transgenic plants, comprises  
 PT transforming a plant (cell) with an expression construct having nitrogen-  
 PT inducible promoter, an open reading frame of a gene and a polyadenylation  
 PT site.

Claim 1; Page 28-29; 44pp; English.

XX AAF84905-17 represent nitrogen-inducible promoters. They are promoters of  
 CC the nitrite reductase (Nir) gene. The promoter is used for regulating  
 CC foreign gene transcription in transgenic organisms. The method uses an  
 CC expression construct having a nitrogen-inducible promoter, with(out) cis-  
 CC acting sequence, operably linked to the gene to be expressed and  
 CC modulated for transcriptional expression of the gene by addition or  
 CC removal of a nitrogen inducer, an open reading frame of a gene, and a 3'  
 CC polyadenylation signal. The method is useful for regulating the  
 CC transcription of transgenes in genetically modified organisms. The  
 CC nitrogen-inducible expression cassettes are useful for the controlling  
 CC expression of foreign genes in plants

XX Sequence 3714 BP; 1166 A; 645 C; 649 G; 1254 T; 0 U; 0 Other;

Query Match 9.5%; Score 209.4; DB 4; Length 3714;

Best Local Similarity 66.5%; Pred. No. 7.9e-45;

Matches 341; Conservative 0; Mismatches 151; Indels 21; Gaps 2;

Qy	1486	AGGCTAGCAATTTAACTCTGAATGCTGTGAAGGCTGCTGTGTTTGAAGTTCACATCC	1545
Db	909	AGATCTAGCAATTTAACTCTGAAGGCTGTGTTTGAAGTTCACATCC	968
Qy	1546	CTGAATCTGTGCTGTATGAAGCTGAAGGCTGAAGTATAAGAGGGGGAGTCT	1605
Db	969	CTGAATCATGTTCTGTATGAAGCTGAAGGCTGAAGTATAAGAGGGGGAGTCT	1028
Qy	1606	TTAAACTCTCAAAATATACCAATGCTGTGACAGACAGACAGCTCTTTATACCTTC	1665
Db	1029	TTGAAGGTTTACAAATATACCTGCGGCTTGACAGAGGCAAGCTCTTTATACCTTC	1088
Qy	1666	AGCTTCAAGTGTGCTGTATGAAGCTGAAGGCTGAAGTATAAGAGGGGGAGTCT	1725
Db	1089	CAGTTCACAGGGGATGTTGATTTTCAAGTCACTTTGAGAGCAATCTTTATACCTTC	1148
Qy	1726	GAAGTCAATTTTGTGTAGCATGCGCTAA-----ATGGTACCTCTGCTACCTGAAT	1778
Db	1149	GAAGTAAATTTTGTGTAGCATGTTGAGTACCTTACATGATCATCAGTACAT	1208
Qy	1779	AGCTTCACTTACCTAGCAGCACTAGTATGAGTATGAGTATGAGTATGAGTATGAGT	1838
Db	1209	AGCTCTTTTCACTTAACTAGAGCAATGAAGTATGAGTATGAGTATGAGTATGAGT	1268
Qy	1839	ATGGCTT-----TATTTATGCTAGTCTTCTGGCCAACTCATTTGATGTTT	1884
Db	1269	ATGGCTTGTGATGCTACCTTCTGGCCAACTCATCGGGGATTTACATTCAGAAAT	1328
Qy	1885	GTATAAGACATCACACTTTAAATTTTAACTTGTCTGTAGAAGTGCATATTTA	1944

Db	1329	ATACATGACTTCAACCATACCTTAAACCCCTTTTCTGAAGATAAATGAATGTTTCATATTTA	1388
QY	1945	ATGCTTAGTCTTATGCTCTTATCTGATCATCT	1977
Db	1389	ATGTTGGGTGTAGTGTGTTTACTTGATATAT	1421
RESULT 15			
AD38881	AAD38881 standard; DNA; 3775 BP.		
XX	AC	AAD38881;	
XX	DT	23-SEP-2002 (first entry)	
XX	DE	Alfalfa AP2 adaptor with nitrite reductase gene (Nir) promoter.	
XX	XX	Expression regulatory sequence; recombinant polypeptide; gene cloning;	
KW	alfalfa; nitrite reductase gene; Nir; AP2 adaptor; ds.		
XX	OS	Medicago sativa.	
XX	PN	WO200236786-A2.	
XX	PD	10-MAY-2002.	
XX	PF	31-OCT-2001; 2001WO-CA001532.	
XX	PR	31-OCT-2000; 2000US-0244214P.	
XX	PA	(MEDI-) MEDICAGO INC.	
XX	PI	Vezina L, D'aoust M, Arcand F, Bilodeau P;	
XX	DR	WPI; 2002-471503/50.	
XX	XX	Isolating and characterizing an expression regulatory sequence for	
PT	expressing recombinant polypeptides and/or RNA, comprises producing		
PT	oligonucleotide primers that amplify sequences upstream or downstream of		
PT	CDNAs.		

Search completed: February 19, 2006, 15:54:30  
Job time : 1228 secs

XX	Example 2; Page 67-68; 74pp; English.
PS	The invention relates to a method for isolating and characterising an
XX	expression regulatory sequence for the expression of recombinant
CC	polypeptides and/or RNA. The method comprising producing at least one
CC	oligonucleotide primer from cDNAs of a cDNA library, where the
CC	oligonucleotide primer allows amplification of genomic sequences upstream
CC	or downstream of the cDNAs. The method is useful for isolating,
CC	characterising and identifying a large number of known and unknown
CC	promoters that are active under any desired environmental condition to
CC	which a cell may be exposed and not just to the exemplified isolation of
CC	promoters that are capable of expression in specific conditions. The
CC	methods are also useful for cloning genes from any host, or from a
CC	specific tissue with such host, from which a cDNA library may be
CC	constructed; for the identification and isolation of analogous promoters,
CC	signal peptides and structural genes in several species of multicellular
CC	and unicellular organisms and as a high throughput identification system
CC	of candidate therapeutic targets. The promoter sequences may be used to
CC	regulate the synthesis of polypeptides. The present sequence is alfalfa
CC	AP2 adapter with nitrite reductase gene (Nir)
XX	Sequence 3775 BP; 1180 A; 658 C; 670 G; 1267 T; 0 U; 0 Other;
SQ	
Query Match	
Best Local Similarity 9.5%; Score 209.4; DB 6; Length 3775;	
Matches 341; Conservative 0; Mismatches 151; Indels 21; Gaps 2;	
QY	1486 AGGCTAGCAATTTAACTCTGAAGCTGCTGTGTTGTTGAAAGTTCCACATCC 1545
Db	957 AGATCTAGCAATTTAACTCTGAGTCTCTTCAAGAGTCTGTTCTACGAAGTTCCAGTCC 1016
QY	1546 CTGAATCTTGTGCTGTATGAAGACTGAAAGCCCTGAAGTTATTAAGAGGGGGAGTCT 1605



```

Db      410 GAAAGTAAATTTTGTGTAGCATATGTTGAGCTACCTACCAATTTACATGATCACCTAGCAAT 469
Qy      1779 AGCTTCACTAGCTAGCAGCACTAGCTAGAGTTTATAGGAATGAGTATGGCAGTGAATATATGCG 1838
Db      470 AGCTCTTTTCACTAACTGAGAGAAATGAAGTTTATAGGAATGAGTATGACCAATGGAGTCGGC 529
Qy      1839 ATGGCTT-----TATTTATGCGCTAGTGTCTTCTGGCCAACTCAATGATGTTTT 1884
Db      530 ATGGCTTTGTAATGCTACCCCTACTTTGGCCAACTCATCGGGATTTACATTCAGAAAT 589
Qy      1885 GTATAAGACATCACACTTTTAAATTTTAAACTTGTCTGTAGAAAGTGCATAATCCATATTTA 1944
Db      590 ATACATGACTTCAACCATACTTAAACCCCTTTTGTAGATAAATACTGAATGTTTATATTTA 649
Qy      1945 ATGCTTAGTTTATGCTCTTATCTGATCATCT 1977
Db      650 ATGTTGGGTTGTAGTGTTTTACTTGATTATAT 682

```

# RESULT 2

```

US-09-678-300-6
; Sequence 6, Application US/09678300
; Patent No. 6420548
; GENERAL INFORMATION:
; APPLICANT: VOZINA, Louis-Philippe
; APPLICANT: D'Aoust, Marc-Andr 
; APPLICANT: MEDICAGO INC.
; TITLE OF INVENTION: METHOD FOR REGULATING TRANSCRIPTION OF
; FILE REFERENCE: 14149-3"PCT"
; CURRENT APPLICATION NUMBER: US/09/678,300
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 1999-10-04
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 2124
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sequences to be used as promoter for regulating
; OTHER INFORMATION: expression of foreign genes
US-09-678-300-6

```

```

Query Match      9.5%; Score 209.4; DB 3; Length 2124;
Best Local Similarity 66.5%; Pred. No. 1.5e-50;
Matches 341; Conservative 0; Mismatches 151; Indels 21; Gaps 2;

Qy      1486 AGGCTAGCAATTTAACTCTGAATGCTGTGAAGGCTGCTGTGTTTGAAGTTTCAATCC 1545
Db      170 AGATCTAGCAATTTAACTCTGGAGTCTTCAAGACTGCTGTCTTACGAAGTTTCACTGCC 229
Qy      1546 CTGAATCTTGCTGTATGGAAGCTGAAAGGCTCAAGTTTAAAGAGGGGGAGTGCT 1605
Db      230 CTGAATCATGTTCTGTATGGAAGCTGAAAGACCTCAAATTTAAAGGTGGCGATAAA 289
Qy      1606 TTAATACTCTACAAAATATACCCAAATTTGGCTTGACACAGAGACAAGCTCTTTATACCTTC 1665
Db      290 TTGAAGGTTTACAAAATATACCTCGGGCTTGACACAGAGCAAGCTCTTTATACCTTC 349
Qy      1666 AGCTTCAAAAGGTGATGCTGATTTCAAGAGTCACTTGGAGAGCAATCTCTGTGCGCAAGTTT 1725
Db      350 CAGTTTCAACGGGATGTTGATTTTCAAGAGTCACTTGGAGAGCAATCTCTGTGCGCAAGTTT 409
Qy      1726 GAAGTCAATTTTGTAGCATGCGCTAA-----ATGGTACCTCTGCTCTACCTGAATT 1778
Db      410 GAAGTAAATTTTGTAGCATATGTTGAGCTACTCAAATTTACATGATCACCTAGCAAT 469
Qy      1779 AGCTTCACTAGCTAGCAGCACTAGCTAGAGTTTATAGGAATGAGTATGGCAGTGAATATGCG 1838
Db      470 AGCTTCACTAGCTAGCAGCACTAGCTAGAGTTTATAGGAATGAGTATGGCAGTGAATATGCG 529
Qy      1839 ATGGCTT-----TATTTATGCGCTAGTGTCTTGGCCAACTCAATGATGTTTT 1884
Db      530 ATGGCTTTGTAATGCGCTACCCCTACTTTGGCCAACTCATCGGGATTTTACATTCAGAAAT 589
Qy      470 AGCTCTTTTCACTAACTGAGAGAAATGAAGTTTATAGGAATGAGTATGACCAATGGAGTCGGC 529

```

```

Qy      1839 ATGGCTT-----TATTTATGCGCTAGTGTCTTGGCCAACTCAATGATGTTTT 1884
Db      530 ATGGCTTTGTAATGCGCTACCCCTACTTTGGCCAACTCATCGGGATTTTACATTCAGAAAT 589
Qy      1885 GTATAAGACATCACACTTTTAAATTTTAAACTTGTCTGTAGAAAGTGCATAATCCATATTTA 1944
Db      590 ATACATGACTTCAACCATACTTAAACCCCTTTTGTAGATAAATACTGAATGTTTATATTTA 649
Qy      1945 ATGCTTAGTTTATGCTCTTATCTGATCATCT 1977
Db      650 ATGTTGGGTTGTAGTGTTTTACTTGATTATAT 682

```

# RESULT 3

```

US-09-678-300-9
; Sequence 9, Application US/09678300
; Patent No. 6420548
; GENERAL INFORMATION:
; APPLICANT: VOZINA, Louis-Philippe
; APPLICANT: D'Aoust, Marc-Andr 
; APPLICANT: MEDICAGO INC.
; TITLE OF INVENTION: METHOD FOR REGULATING TRANSCRIPTION OF
; FILE REFERENCE: 14149-3"PCT"
; CURRENT APPLICATION NUMBER: US/09/678,300
; CURRENT FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: US 60/157,133
; PRIOR FILING DATE: 1999-10-04
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 2165
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sequences to be used as promoter for regulating
; OTHER INFORMATION: expression of foreign genes
US-09-678-300-9

```

```

Query Match      9.5%; Score 209.4; DB 3; Length 2165;
Best Local Similarity 66.5%; Pred. No. 1.5e-50;
Matches 341; Conservative 0; Mismatches 151; Indels 21; Gaps 2;

Qy      1486 AGGCTAGCAATTTAACTCTGAATGCTGTGAAGGCTGCTGTGTTTGAAGTTTCAATCC 1545
Db      170 AGATCTAGCAATTTAACTCTGGAGTCTTCAAGACTGCTGTCTTACGAAGTTTCACTGCC 229
Qy      1546 CTGAATCTTGCTGTATGGAAGCTGAAAGGCTGAAAGCTTATAAGAGGGGGAGTGCT 1605
Db      230 CTGAATCATGTTCTGTATGGAAGCTGAAAGACCTCAAATTTAAAGGTGGCGATAAA 289
Qy      1606 TTAATACTCTACAAAATATACCCAAATTTGGCTTGACACAGAGACAAGCTCTTTATACCTTC 1665
Db      290 TTGAAGGTTTACAAAATATACCTCGGGCTTGACACAGAGCAAGCTCTTTATACCTTC 349
Qy      1666 AGCTTCAAAAGGTGATGCTGATTTCAAGAGTCACTTGGAGAGCAATCTCTGTGCGCAAGTTT 1725
Db      350 CAGTTTCAACGGGATGTTGATTTTCAAGAGTCACTTGGAGAGCAATCTCTGTGCGCAAGTTT 409
Qy      1726 GAAGTCAATTTTGTAGCATGCGCTAA-----ATGGTACCTCTGCTCTACCTGAATT 1778
Db      410 GAAGTAAATTTTGTAGCATATGTTGAGCTACTCAAATTTACATGATCACCTAGCAAT 469
Qy      1779 AGCTTCACTAGCTAGCAGCACTAGCTAGAGTTTATAGGAATGAGTATGGCAGTGAATATGCG 1838
Db      470 AGCTTCACTAGCTAGCAGCACTAGCTAGAGTTTATAGGAATGAGTATGGCAGTGAATATGCG 529
Qy      1839 ATGGCTT-----TATTTATGCGCTAGTGTCTTGGCCAACTCAATGATGTTTT 1884
Db      530 ATGGCTTTGTAATGCGCTACCCCTACTTTGGCCAACTCATCGGGATTTTACATTCAGAAAT 589
Qy      1885 GTATAAGACATCACACTTTTAAATTTTAAACTTGTCTGTAGAAAGTGCATAATCCATATTTA 1944

```





```

; FILE REFERENCE: 14149-3"PCT"
; CURRENT APPLICATION NUMBER: US/09/678,300
; CURRENT FILING DATE: 2000-10-03
; PRIOR FILING DATE: 1999-10-04
; PRIOR FILING DATE: 1999-10-04
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 2904
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sequences to be used as promoter for regulating
; OTHER INFORMATION: expression of foreign genes
US-09-678-300-8

Query Match          9.5%; Score 209.4; DB 3; Length 2904;
Best Local Similarity 66.5%; Pred. No. 1.8e-50;
Matches 341; Conservative 0; Mismatches 151; Indels 21; Gaps 2;

QY 1486 AGGCTAGCAATTTAACTCTGAATGCTGTAAGGCTGCTGTTGTTGAAAGTTTCAATCC 1545
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 909 AGATCTAGCAATTTAACTCTGAGTCTCTCAAGACTGCTGTTCTTACGAAGTTCACTGCC 968
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1546 CTGAATCTTGCTGCTGTATGGAAGACTGAAAGGCTGAAGTTATAAGAGGGGGAGTGCT 1605
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 969 CTGAATCATGTTCTGTATGGAAGCTGAAAGACCTCAAAATTTCTAAAAGGTGGCGATAAA 1028
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1606 TTAAACTCTACAAAATATACCCAAATTTGGCTTTGACACAGAGACAAGCTCTTTATACCTTC 1665
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1029 TTGAAGTTTACAAAATATACCTCGCGGCTTGACACAGAGCAAGCTCTTTATACCTTC 1088
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1666 AGCTTCAAAGGTGATGCTGATTTCAAGAGTCACTTGGAGAACAACTCTTGCCCAAGTTT 1725
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1089 CAGTTCAAAGGGGATGTTGATTTTCAAGAACTCACTTGGAGAGCAATCTTGTGCCAAGTTT 1148
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1726 GAAGTCATTTTGTGTAGCATGCGCTAA-----ATGCTACCTCTGCTCTACCTGAAT 1778
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1149 GAAGTAAATTTTGTGTAGCATATGTTGAGCTACCTACCTACCAATTTACATGATCACCTAGCA 1208
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1779 AGCTTCACTTAGCTAGCACTAGCTAGAGTATGAGTATGAGTATGAGTATGAGTATGAGTATGAG 1838
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1209 AGCTTCTTCACTTAAGTGAAGTAAAGTTTGAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 1268
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1839 ATGGCTT-----TATTTATGCTAGTTCTTATCTGATCATCT 1884
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1269 ATGGCTTTGTAATGCTACCTACCTACCTACCTACCTACCTACCTACCTACCTACCTACCTACCT 1328
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1885 GTATAAGACATCACACTTTAAATTTTAACTTTTAACTTTTAACTTTTAACTTTTAACTTTTAA 1944
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1329 ATACATGACTTCAACCACTACTTAAACCCCTTTTGTAAAGTAACTGAATGTTTCAATATTA 1388
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1945 ATGCTTAGTTTGTAGTCTCTTATCTGATCATCT 1977
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1389 ATGTTGGTGTAGTGTGTTTACTTATATAT 1421
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 8
US-09-678-300-11
; Sequence 11, Application US/09678300
; Patent No. 6420548
; GENERAL INFORMATION:
; APPLICANT: VOZINA, Louis-Philippe
; APPLICANT: D'AROUS, Marc-Andr,
; APPLICANT: MEDICAGO INC.
; TITLE OF INVENTION: METHOD FOR REGULATING TRANSCRIPTION OF
; FILE REFERENCE: 14149-3"PCT"
; CURRENT APPLICATION NUMBER: US/09/678,300
; CURRENT FILING DATE: 2000-10-03
; PRIOR FILING DATE: 1999-10-04
; NUMBER OF SEQ ID NOS: 32

```

```

; FILE REFERENCE: 14149-3"PCT"
; CURRENT APPLICATION NUMBER: US/09/678,300
; CURRENT FILING DATE: 2000-10-03
; PRIOR FILING DATE: 1999-10-04
; PRIOR FILING DATE: 1999-10-04
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 2863
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sequences to be used as promoter for regulating
; OTHER INFORMATION: expression of foreign genes
US-09-678-300-5

Query Match          9.5%; Score 209.4; DB 3; Length 2863;
Best Local Similarity 66.5%; Pred. No. 1.8e-50;
Matches 341; Conservative 0; Mismatches 151; Indels 21; Gaps 2;

QY 1486 AGGCTAGCAATTTAACTCTGAATGCTGTAAGGCTGCTGTTGTTGAAAGTTTCAATCC 1545
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 909 AGATCTAGCAATTTAACTCTGAGTCTCTCAAGACTGCTGTTCTTACGAAGTTCACTGCC 968
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1546 CTGAATCTTGCTGCTGTATGGAAGACTGAAAGGCTGAAGTTATAAGAGGGGGAGTGCT 1605
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 969 CTGAATCATGTTCTGTATGGAAGCTGAAAGACCTCAAAATTTCTAAAAGGTGGCGATAAA 1028
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1606 TTAAACTCTACAAAATATACCCAAATTTGGCTTTGACACAGAGACAAGCTCTTTATACCTTC 1665
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1029 TTGAAGTTTACAAAATATACCTCGCGGCTTGACACAGAGCAAGCTCTTTATACCTTC 1088
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1666 AGCTTCAAAGGTGATGCTGATTTCAAGAGTCACTTGGAGAACAACTCTTGCCCAAGTTT 1725
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1089 CAGTTCAAAGGGGATGTTGATTTTCAAGAACTCACTTGGAGAGCAATCTTGTGCCAAGTTT 1148
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1726 GAAGTCATTTTGTGTAGCATGCGCTAA-----ATGCTACCTCTGCTCTACCTGAAT 1778
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1149 GAAGTAAATTTTGTGTAGCATATGTTGAGCTACCTACCAATTTACATGATCACCTAGCA 1208
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1779 AGCTTCACTTAGCTAGCACTAGCTAGAGTATGAGTATGAGTATGAGTATGAGTATGAGTATGAG 1838
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1209 AGCTTCTTCACTTAAGTGAAGTAAAGTTTGAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 1268
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1839 ATGGCTT-----TATTTATGCTAGTTCTTATCTGATCATCT 1884
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1269 ATGGCTTTGTAATGCTACCTACCTACCTACCTACCTACCTACCTACCTACCTACCTACCTACCT 1328
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1885 GTATAAGACATCACACTTTAAATTTTAACTTTTAACTTTTAACTTTTAACTTTTAACTTTTAA 1944
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1329 ATACATGACTTCAACCACTACTTAAACCCCTTTTGTAAAGTAACTGAATGTTTCAATATTA 1388
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1945 ATGCTTAGTTTGTAGTCTTATCTGATCATCT 1977
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1389 ATGTTGGTGTAGTGTGTTTACTTATATAT 1421
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 7
US-09-678-300-8
; Sequence 8, Application US/09678300
; Patent No. 6420548
; GENERAL INFORMATION:
; APPLICANT: VOZINA, Louis-Philippe
; APPLICANT: D'AROUS, Marc-Andr,
; APPLICANT: MEDICAGO INC.
; TITLE OF INVENTION: METHOD FOR REGULATING TRANSCRIPTION OF
; FILE REFERENCE: 14149-3"PCT"
; CURRENT APPLICATION NUMBER: US/09/678,300
; CURRENT FILING DATE: 2000-10-03
; PRIOR FILING DATE: 1999-10-04
; NUMBER OF SEQ ID NOS: 32

```

```

; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 2971
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sequences to be used as promoter for regulating
; OTHER INFORMATION: expression of foreign genes
US-09-678-300-11

Query Match          9.5%; Score 209.4; DB 3; Length 2971;
Best Local Similarity 66.5%; Pred. No. 1.8e-50;
Matches 341; Conservative 0; Mismatches 151; Indels 21; Gaps 2;

1486 AGGCTCTAGCAATTTAACTCTGAATGCTGTGAAGGCTGCTGTTGTTTGAAGTTTCACATCC 1545
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
909 AGATCTAGCAATTTAACTCTGGAGTCTCTCAAGACTGCTGTTCTTACGAAGTTTCACGTC 968
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1546 CTGAATCTTTGTGCTGTATGGAAGACTGAAAGCCCTGAAAGTTTATAGAGGGGGAGTGCT 1605
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
969 CTGAATCATGTTCTGTATGGAAGCTGAAAGACCTCAAAATCTTAAAGGTGGCGATAAA 1028
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1606 TTAAGACTCTCAAAAATATACCAATTTGGCTTGACACAGAGCAAGCTCTTTATACCTTC 1665
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1029 TTGAAGGTTTACAAAATATACCTCGGGCTTGACACAGAGGCAAGCTCTTTATACCTTC 1088
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1666 AGCTTCAAGGTTGATGCTGATTTTCAAGAGTCACTTGGAGAACAACTCTTGCCCAAGTTT 1725
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1089 CAGTTCAACGGGAGTGTGATTTTCAAGACTCACTTGGAGCAATCTTGCCCAAGTTT 1148
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1726 GAAGTCATTTTGTGAGCATGCGCTAA-----ATGGTACCTCTGCTCTACCTGAAT 1778
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1149 GAAGTAAATTTTGTGAGCATATGTTAGCTACCTACAAATTTACATGATCACCTAGCAT 1208
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1779 AGCTTCACCTAGCTAGCACTAGCTAGAGTTTGTAGGAATGAGTATGGCAGTGAATATGCG 1838
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1209 AGCTCTTTTCACTTAACTGAGAAATGAAGTTTGTAGGAATGAGTATGACCATGGAGTCGCG 1268
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1839 ATGGCTT-----TATTTATGCTAGTTTCTTGCCCAACTCATCTGATGATGTTT 1884
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1269 ATGGCTTTGTAATGCTACCTACTTTGGCCAACTCATCGGGAATTTACATCAGAAAT 1328
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1885 GTATAAGACATCACACTTTAAATTTTAACTTCTGTAGAGTGCAAAATCCATATTTA 1944
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1329 ATACATGACTTCAACCATACTTAAACCCCTTTTGTAGAACTGAATGTTTCATATTTA 1388
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1945 ATGCTTAGTTTGTAGTCTCTTATCTGATCATCT 1977
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1389 ATGTTGGGTTGATGTTTACTTGAATATAT 1421
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

```

RESULT 9
US-09-678-300-1
; Sequence 1, Application US/09678300
; Patent No. 6420548
; GENERAL INFORMATION:
; APPLICANT: VOZINA, Louis-Philippe
; APPLICANT: D'AROUT, Marc-Andr ,
; APPLICANT: MEDICAGO INC.
; TITLE OF INVENTION: METHOD FOR REGULATING TRANSCRIPTION OF
; FILE REFERENCE: 14149-3"PC"
; CURRENT APPLICATION NUMBER: US/09/678,300
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: US 60/157,133
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 3714
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

```

```

; OTHER INFORMATION: Sequences to be used as promoter for regulating
; OTHER INFORMATION: expression of foreign genes
US-09-678-300-1

Query Match          9.5%; Score 209.4; DB 3; Length 3714;
Best Local Similarity 66.5%; Pred. No. 2.1e-50;
Matches 341; Conservative 0; Mismatches 151; Indels 21; Gaps 2;

1486 AGGCTCTAGCAATTTAACTCTGAATGCTGTGAAGGCTGCTGTTTGAAGTTTCACATCC 1545
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
909 AGATCTAGCAATTTAACTCTGGAGTCTCTCAAGACTGCTGTTCTTACGAAGTTTCACGTC 968
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1546 CTGAATCTTTGTGCTGTATGGAAGACTGAAAGCCCTGAAAGTTTATAGAGGGGGAGTGCT 1605
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
969 CTGAATCATGTTCTGTATGGAAGCTGAAAGACCTCAAAATCTTAAAGGTGGCGATAAA 1028
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1606 TTAAGACTCTCAAAAATATACCAATTTGGCTTGACACAGAGCAAGCTCTTTATACCTTC 1665
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1029 TTGAAGGTTTACAAAATATACCTCGGGCTTGACACAGAGGCAAGCTCTTTATACCTTC 1088
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1666 AGCTTCAAGGTTGATGCTGATTTTCAAGAGTCACTTGGAGAACAACTCTTGCCCAAGTTT 1725
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1089 CAGTTCAACGGGAGTGTGATTTTCAAGACTCACTTGGAGCAATCTTGCCCAAGTTT 1148
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1726 GAAGTCATTTTGTGAGCATGCGCTAA-----ATGGTACCTCTGCTCTACCTGAAT 1778
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1149 GAAGTAAATTTTGTGAGCATATGTTAGCTACCTACAAATTTACATGATCACCTAGCAT 1208
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1779 AGCTTCACCTAGCTAGCACTAGCTAGAGTTTGTAGGAATGAGTATGGCAGTGAATATGCG 1838
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1209 AGCTCTTTTCACTTAACTGAGAAATGAAGTTTGTAGGAATGAGTATGACCATGGAGTCGCG 1268
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1839 ATGGCTT-----TATTTATGCTAGTTTCTTGCCCAACTCATCTGATGATGTTT 1884
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1269 ATGGCTTTGTAATGCTACCTACTTTGGCCAACTCATCGGGAATTTACATCAGAAAT 1328
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1885 GTATAAGACATCACACTTTAAATTTTAACTTCTGTAGAGTGCAAAATCCATATTTA 1944
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1329 ATACATGACTTCAACCATACTTAAACCCCTTTTGTAGAACTGAATGTTTCATATTTA 1388
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1945 ATGCTTAGTTTGTAGTCTCTTATCTGATCATCT 1977
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1389 ATGTTGGGTTGATGTTTACTTGAATATAT 1421
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

```

Query Match          2.2%; Score 47.8; DB 3; Length 1141;
Best Local Similarity 10.3%; Pred. No. 0.0029;
Matches 68; Conservative 255; Mismatches 335; Indels 0; Gaps 0;

```

QY	1416	AGGCCAGAAA	CCGTATATCATCATCTATCTCAGAGAAAGGGGAAGGTTTGAGATGAGGTC	1475
Db	53	MSKSRKWTTWARM7CKYTRRWNKSRWKGWYKKWYBCANN7TSBRVHARRWKMKTAYBM	112	
QY	1476	CATT7TACCTGAGGCTCTAGCAATTTAACTCTGTAATGCTGTAAGGCTGCTGTTGTTTGA	1535	
Db	113	TWINKGKTGWRHRYWKRAMB7VDVHHVVTAMNNAW7TMCMMDKDKRTRWKKNNNA	172	
QY	1536	GTTTCAATCCCTGAATCTTGTGCTCTGTAAGAGACTGAAAGGCTCGAAGTTTATAAGAG	1595	
Db	173	TGWD7DDTKYHMMNNNGCBVTWVMVRYKTRDWSBKRMYGMBWKKWS7DV7YYWVWDD	232	
QY	1596	GGGAGGTCCTTTAA7AACTCTACAAAATATACCAA7TGGCTTGACACAGAGACAAGCTCT	1655	
Db	233	MCKRKVPRVYR7RGRMENVYVAM7BTAHRRRYNNGWTBAMAYR7RWTWNNNNNNAKAKCKRA	292	
QY	1656	TTATACCTTCAGCTTC7CAAAGGTGATGCTGATTT7CAGAG7CAC7TTCGAGAACAA7CCTTG	1715	
Db	293	KYMGWNRABVNSTCTTWKSK7T7KVRTSCWANNCRAGDANKDKHKKWKSAA7GVYNNNN	352	
QY	1716	TGCCAAAGTT7TGAAGTCATATTT7TGTAGCATGCGCTAAAT7GGTACCTCTGCTCTACTGA	1775	
Db	353	NNW7YKKARBEAR7MDW7HSAWKKWHA7AAH7SRKKWTBYKRKTMTWNNNGTT7TWKRMWA	412	
QY	1776	ATTAGCTTC7TAC7TAC7GACCATAGCTAGAGTT7TTTAGGAATGAG7ATGCGACGTGAAT	1835	
Db	413	WY7KMD7MD7BGT7YNNNGG7TY7G7W7K7K7M7Y7Y7K7KANNCKWRAD7DKT7CHN7TW	472	
QY	1836	GGCATGGCT7TTAT7TATGCCTAG7TCTTCTTGCCAACTCAT7GATGTTTGTATAAGACAT	1895	
Db	473	WK7KTYNN7CY7K5W7NG7KSHRBA7AA7V7TW7MMW7RY7AH7ANN7ND7W7K7ACTW7KYVB	532	
QY	1896	CACACTTTAA7TTTAA7CTGTTCT7TGTAGAAG7GCAAA7CCA7TAT7TAATGCTTAGTTT	1955	
Db	533	CS7KWN7NYAA7YT7K5S7WN7Y7RY7RW7K7NN7SR7WRSD7RS7MGRANN7YAR7AH7Y7K7W7NR	592	
QY	1956	TAG7GCTCT7TATCTCATCT7CAGAAG7CACAG7TCT7TGTATAT7TGTAG7G7G7AA7ACTGA	2015	
Db	593	WW7BS7HT7WB7H7RAGA7AA7W7MM7BY7BAK7CH7C7KAW7Y7KAK7Y7AG7GS7NN7NN7NN7NN	652	
QY	2016	AATCTAA7TGA7AGGATCAGATGTT7TCTCA7GACACAT7TAT7TACT7CATCTGTTT	2073	
Db	653	NNATCARD7DY7AAS7SW7Y7AWAK7W7YY7Y7K7BA7NNA7Y7T7H7N7W7G7W7NNA7T7R7ET7MWK	710	

RESULT 11  
US-08-737-524B-1  
; Sequence 1, Application US/08737524B  
; Patent No. 5912414  
; GENERAL INFORMATION:  
; APPLICANT: CARL SAVERIO FALCO  
; APPLICANT: DOMINICK ANTHONY GUIDA, JR.  
; APPLICANT: MARY ELIZABETH HARNETT LOCKE  
; TITLE OF INVENTION: NUCLEIC ACID FRAGMENTS, CHIMERIC  
; TITLE OF INVENTION: GENES AND METHODS FOR INCREASING  
; TITLE OF INVENTION: THE METHIONINE CONTENT OF THE SEEDS  
; TITLE OF INVENTION: OF PLANTS  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY  
; STREET: 1007 MARKET STREET  
; CITY: WILMINGTON  
; STATE: DELAWARE  
; COUNTRY: UNITED STATES OF AMERICA  
; ZIP: 19898  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: DISKETTE, 3.50 INCH  
; COMPUTER: IBM PC COMPATIBLE  
; OPERATING SYSTEM: MICROSOFT WINDOWS 95  
; SOFTWARE: MICROSOFT WORD FOR WINDOWS 95 (7.0)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/737,524B  
; FILING DATE:

```

CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: LYNNE M. CHRISTENBURY
REGISTRATION NUMBER: 30,971
REFERENCE/DOCKET NUMBER: BB-1059-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-5481
TELEFAX: 302-773-0164
TELEX: 835420
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1639 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 2..1441
US-08-737-524B-1

Query Match          2.0%; Score 44.4; DB 2; Length 1639;
Best Local Similarity 55.1%; Pred. No. 0.036;
Matches      87; Conservative    0; Mismatches     71; Indels       0; Gaps        0;

Qy   2041  CACTCAGACACATTTACTTCATCTGCTTTTGATGATCATCGAGCTTTTTTGTAGTGTCTG 2100
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db   1446  CACTCTAAATCAGTTTGTATTGCACAAATCATGAGGTGATGGCTGCTTGTGATCTTGTCAA 1505
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy   2101  GAATCTGCCCTGTGGTTTGTGACCACTGTTATTGCTTCAGTGTACTGTCCAGTGGTTATC 2160
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db   1506  GATCTGTGCAATGATATGAGCTGATGACGCGCAATAAGTTCTCTTTTGTCTATTATTATC 1565
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy   2161  GTTTTTGACCTCTAAAAAAAAAAAAAAAAAAAAAAAA 2198
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db   1566  CGTCAAAATTCAAAAAATAAAAAAAAAAAAAAAAAAAAAAAA 1603
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

## RESULT 12

```

US-09-806-708B-22/c
; Sequence 22, Application US/09806708B
; Patent No. 6784342
; GENERAL INFORMATION:
; APPLICANT: The University of British Columbia
; TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants
; FILE REFERENCE: 4810-58741
; CURRENT APPLICATION NUMBER: US/09/806,708B
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/147,133
; PRIOR FILING DATE: 1999-08-04
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 1141
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(1141)
; OTHER INFORMATION: consensus sequence of A.t., L.a., and B.n. PAEI promoters
US-09-806-708B-22

```

Query Match	2.0%	Score 43.6;	DB 3;	Length 1141;
Best Local Similarity	11.3%;	Pred. No. 0.049;		
Matches 117;	Conservative 357;	Mismatches 555;	Indels 4;	Gaps 2;
Qy	1160	GTTCAATTTTACATATATAAGACATAGAGGATCTTGAGTCTGTGGCAAGACCACATGAGAT	1219	
Db	1132	GNTTTTKTKYKANNNNNNNGMGKDNRMDATKWSATGTAWNTNHAKRGAATMCWYWT	1073	
Qy	1220	ATCTAGCAGAAATCCCGAAGCATATAATCAATCATTGAGGTGGAAGTATGAGGGTCCAT	1279	
Db	1072	GTNRRCMRTYAMRTWYTRSNANWSATKEHWTKMKYATKYRTAWYAMWCARNNNNWC	1013	

```

Qy 1280 CTGACTCCTTCAAGCCCTTGTGATATGGCAGCTGTGCTTCAATCATCGTGGCTTTGCA 1339
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 1012 ATNGTAKSCATNNMTATTRWAAAYAAKWARWAGNNWMTYGAAGNKGOMAAATMGB 953
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 1340 TTCACCTTGGCCACAGTGTAGTACAGAGAGAGAAATAATCCAAAGCCTTAAAGAGCGTC 1399
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 952  WADTAGKCMNNNNNTTDDVRWAMKAKNNNNNAVWTCYNRAATNNKMAWTHMKWTH 893
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 1400 CTTGCAAGTGCATAGAGGGCCAGAAACCGTATATCATATCTATGTCAGAGAAAGGGAA 1459
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 892  GAHSKRTRHTRTCTRTKYNNNNNNARTVYVYHAAARRWNNWMTTNNNNNNNNNAC 833
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 1460 GGTTTGAGATGGAGCTTACCTGAGGTCTACCAATTTAACTCTCAATGCTGCTGAAGG 1519
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 832  RNTRT---WWABVKSNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 776
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 1520 CTGCTGTGTTTGAAGTTTCACTCCCTGCTGATCTGTGCTGTATGGAAGCTGAAAGGC 1579
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 775  CNYMHAATVTHTDWCYKTMNTWYDMMTMBTTTTNNNNNNNNNNNNNNNNNNNNNN 716
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 1580 CTGAAGTTATAAGAGGGGAGTCTTTAACTCTACAAATATATCCCAATGCGGTGA 1639
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 715  NNNNNMKAYYAHATNNWGWNTDARRTNNNTVMRRRWNTKTRWYSTTRHHYTG 656
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 1640 CACAGACAGCTCTTTATACCTTACCTTCAAGCTGATGCTGATTTTCAGGAGTCACT 1699
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 655  TNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 596
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 1700 -TGAGAACAACTCTGTGCAAGTTTGAAGTCAATTTTGTGTAGCATGGCTAAATGGT 1758
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 595  VWYVAMRCBDVTYTRNNYCKSYAHYVWNSNNAMWYRYSARNSMARWTRNNW 536
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 1759 ACCTCTCTCTACCTAATAGCTTCTTACCTAGCTGAGCACCTAGCTAGGATTTAGGAATG 1818
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 535  MSGBVRMRWAGTMMWRHNNNTDTRYVWKKWARBTTVYDSMCAKSMWRGNWRAM 476
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 1819 AGTATGCGAGTGAATAGCATGCTTTATTTATGCTAGTCTTCTTGGCCCACTCATGA 1878
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 475  KMMVAANDAGAMDHTVYMGNNMMRRRAKMMMAWCCRAYCCNNNNNNRACVWHKHM 416
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 1879 TGTTTGTATAAGACATCACACTTTAAATTTTAAACTTGTCTCTAGAAAGTGCAATCCA 1938
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 415  WRWTKWYKAAACNNNNBKAMVAMWYSDRTTNDMMWTSDBWHWYVDTYWMRA 356
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 1939 TATTTAATGCTAGTCTTGTAGCTCTTATCTGATCATCTAGAACTGACAGTCTTGTATA 1998
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 355  WNNNNNNNRBCKTTSWMMHDMHNTCTYGNNTWGSAYBMAASMMMAAGASNEVTYNWC 296
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 1999 TTGTGAGTGAACACTGAACTTAATAGAGATCAGATGTTTCTCAAGACACATATT 2058
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 295  WRMTYMGKTMNNNNNNKAMTYRTKTVAMCNRYYDTAVMTBKNNKYCYAYBMYBM 236
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 2059 ACTTCATGTTGTTGTATGATCTGAGCTTTTGTAGTCTGGAACCTGCTCCCTGCTGTT 2118
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 235  MGKHHBWRABRSNNWVWKKYVSWHWHAMRYBKABAVGNNWNNKDRMAHH 176
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 2119 GAGCACCTGTATTGCTTGTAGTGTACTGTCTGCTGAGTGTATCGTTTTTGACCTCTAAAA 2178
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 175  WCATNNNNMMWYVYMHMHKHKGAATNNNTABRDDHBAHVKTYYWYRDYWCAMCWN 116
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 2179 AAAAAAATAA 2191
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 115  AKAKVRTAMKHW 103
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

RESULT 13  
 US-09-806-708B-23/c  
 ; Sequence 23, Application US/09806708B  
 ; Patent No. 6784342  
 ; GENERAL INFORMATION:  
 ; APPLICANT: The University of British Columbia  
 ; TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants

; FILE REFERENCE: 4810-58741  
 ; CURRENT APPLICATION NUMBER: US/09/806,708B  
 ; CURRENT FILING DATE: 2001-04-03  
 ; PRIOR APPLICATION NUMBER: US 60/147,133  
 ; PRIOR FILING DATE: 1999-08-04  
 ; NUMBER OF SEQ ID NOS: 23  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 23  
 ; LENGTH: 1055  
 ; TYPE: DNA  
 ; ORGANISM: Artificial sequence  
 ; FEATURE:  
 ; NAME/KEY: promoter  
 ; LOCATION: (1)..(1055)  
 ; OTHER INFORMATION: consensus sequence of A.t. and L.a. PAB1 promoters  
 US-09-806-708B-23

Query Match 1.9%; Score 42.6; DB 3; Length 1055;  
 Best Local Similarity 18.6%; Pred. No. 0.092;  
 Matches 84; Conservative 129; Mismatches 239; Indels 0; Gaps 0;

```

Qy 1575 AAGCCCTGAAGTTTAAAGAGGGGGAGTGTCTTTAAACTCTCAAAATATATACCAATGG 1634
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 477  AAGGYMRAAWAGTWWAAMANNNTTRTYAWWTRWARYTTTRYKSACNAKSMWRGATWRA 418
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 1635 CTTGACACAGACAGACAGCTCTTTATACCTTCAAGCTTCAAAAGGTGATGCTGATTTTCAGGAG 1694
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 417  ATMTTANNKAGAWMMWTTAAGNTWTAAATATMAAAWCAAYCCNNNNWAAACWAMKWM 358
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 1695 TCACCTTGGAGAACAACTCTTGTGCAAGTTTGAAGTCAATTTTGTGTAGCATGCGCTAAA 1754
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 357  WAMTWKYAWGAAACNNNNKTAMYCRRAMWYSAWTTTWWAAATSMWKWYTTTRKTTMAAAA 298
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 1755 TGGTACCTCTGCTCTACCTGAAATAGCTTCACTAGCTAGCTAGCAGTCTAGAGTTTGG 1814
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 297  NNNNNNNWAKCKTTSAMWAMMMMAWCTCGARTWGGATYMAAACCTAAGAGNSMYTCWA 238
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 1815 AATGAGTATGCGAGTGAATATGCGATGGCTTTTATTTATGCTAGTCTTCTTGGCCAACTCA 1874
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 237  ATTGTTTNNNNNNKATWTRTKTMAWCAYYTWTARTYKRYCYATYTYTSMYMGKWM 178
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 1875 TTGATGTTTGTATAAGACATCACCTTTAAATTTTAAACTTGTGTAGAAAGTGCAAA 1934
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 177  WYBARAYASTNCTWSTCRWKTARGWYVAMRYTWTAKASGCGNNNAKWRCAWYACATN 118
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 1935 TCCATATTTAATGCTAGTTTGTAGTCTTATCTGATCATCTAGAAAGTACAGTTCTTG 1994
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 117  NNAMAWYACAYWYTAGKAAWNTNNKTASGKWMYAMMKTTWYWAYWTCACWATAKRR 58
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 1995 TATATTCTGTGAAACTGAAATCTAATAAGA 2026
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 57  TAAKMCWYTRGYMCANNTGRRWAMCAACMAA 26
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

RESULT 14  
 US-08-998-416-185  
 ; Sequence 185, Application US/08998416  
 ; Patent No. 6239264  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Philippsen, Peter  
 ; APPLICANT: Pohlmann, Rainer  
 ; APPLICANT: Steiner, Sabine  
 ; APPLICANT: Mohr, Christine  
 ; APPLICANT: Wendland, Jurgon  
 ; APPLICANT: Knechtle, Philipp  
 ; APPLICANT: Reibschung, Corinne  
 ; TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII  
 ; AND USES THEREOF  
 ; NUMBER OF SEQUENCES: 1152  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESS: NO. 6239264artis Corporation  
 ; STREET: 3054 Cornwallis Road  
 ; CITY: Research Triangle Park

```

; STATE: No. 6239264th Carolina
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/998,416
; FILING DATE: 24-DEC-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: CH 0016/97
; FILING DATE: 31-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
; TELEPHONE: 919-541-8587
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 185:
; LENGTH: 662 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: PAG1073UP
; US-08-998-416-185

Query Match 1.9%; Score 42.4; DB 3; Length 662;
Best Local Similarity 46.9%; Pred. No. 0.08;
Matches 165; Conservative 0; Mismatches 186; Indels 1; Gaps 1;

QY 1845 TTATTTATGCTAGTTTCTTGGCAACTCATTCATGATGTTTTGTATAGACATCACACTTTA 1904
Db 196 TTGATTATTATCTATTAAACATAAAACATTTTAAAAATGTTATAAAATAAATAAGAAATTA 255

QY 1905 ATTTTAACTGTTTCTGTAGAGTCAAAATCCATATTTAATGCTTAGTTTGTAGTGTCT 1964
Db 256 CTTATAGAAATATTATTAAATAGTATTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTT 314

QY 1965 TATCTGATCATCTAGAAAGTCACAGTTCCTGTATATTGTGAGTGAGTCAAAATCTAAATA 2024
Db 315 TATTAAATAAGATATTAAAGTTTAAATATTAAATATTAAATATTAAATATTAAATATTAAATA 374

QY 2025 GAAGGATCAGATGTTTCACCTCAAGACACATATTACTTCACTGTTTGTGATGATCTCGA 2084
Db 375 AATTATTAAATTTACTTCAATGATATATAATTTAAATGATACCTTTTCAATAATATTTA 434

QY 2085 GCTTTTGTAGTCTGGAACGTCCCTGTTGAGCACCTGTTATGCTTCAGTGTTA 2144
Db 435 TTTTATTAGTCTAGTAATAATTTCTATTAAATAGTCTACCTTTTAAATGGATATTACTAC 494

QY 2145 CTGTCAGTGGTATCGTTTGTGACCTCTAAAAAATAAATAAATAAATAAATAAATAA 2196
Db 495 CTACTAAATATTACCTAAATAATATTATTAAAGAAATACCTTAAATCTAAATAA 546

RESULT 15
; Sequence 937, Application US/08998416
; Patent No. 6239264
; GENERAL INFORMATION:
; APPLICANT: Philippsen, Peter
; APPLICANT: Pohlmann, Rainer
; APPLICANT: Steiner, Sabine
; APPLICANT: Mohr, Christine
; APPLICANT: Wendland, Jurgen
; APPLICANT: Knechtle, Philipp

; APPLICANT: Reibischung, Corinne
; TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBVA GOSSVPII
; TITLE OF INVENTION: AND USES THEREOF
; NUMBER OF SEQUENCES: 1152
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6239264artis Corporation
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: No. 6239264th Carolina
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/998,416
; FILING DATE: 24-DEC-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: CH 0016/97
; FILING DATE: 31-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
; TELEPHONE: 919-541-8587
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 185:
; LENGTH: 662 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: PAG1073UP
; US-08-998-416-185

Query Match 1.9%; Score 42.4; DB 3; Length 665;
Best Local Similarity 46.9%; Pred. No. 0.08;
Matches 165; Conservative 0; Mismatches 186; Indels 1; Gaps 1;

QY 1845 TTATTTATGCTAGTTTCTTGGCAACTCATTCATGATGTTTTGTATAGACATCACACTTTA 1904
Db 196 TTGATTATTATCTATTAAACATAAAACATTTTAAAAATGTTATAAAATAAATAAGAAATTA 255

QY 1905 ATTTTAACTGTTTCTGTAGAGTCAAAATCCATATTTAATGCTTAGTTTGTAGTGTCT 1964
Db 256 CTTATAGAAATATTATTAAATAGTATTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTT 314

QY 1965 TATCTGATCATCTAGAAAGTCACAGTTCCTGTATATTGTGAGTGAGTCAAAATCTAAATA 2024
Db 315 TATTAAATAAGATATTAAAGTTTAAATATTAAATATTAAATATTAAATATTAAATATTAAATA 374

QY 2025 GAAGGATCAGATGTTTCACCTCAAGACACATATTACTTCACTGTTTGTGATGATCTCGA 2084
Db 375 AATTATTAAATTTACTTCAATGATATATAATTTAAATGATACCTTTTCAATAATATTTA 434

QY 2085 GCTTTTGTAGTCTGGAACGTCCCTGTTGAGCACCTGTTATGCTTCAGTGTTA 2144
Db 435 TTTTATTAGTCTAGTAATAATTTCTATTAAATAGTCTACCTTTTAAATGGATATTACTAC 494

QY 2145 CTGTCAGTGGTATCGTTTGTGACCTCTAAAAAATAAATAAATAAATAAATAAATAA 2196
Db 495 CTACTAAATATTACCTAAATAATATTATTAAAGAAATACCTTAAATCTAAATAA 546

Search completed: February 19, 2006, 16:13:06
Job time : 401 secs
```

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 19, 2006, 15:45:58 ; Search time 2476 Seconds  
(without alignments)  
7340.910 Million cell updates/sec

Title: US-09-913-858c-1  
Perfect score: 2198  
Sequence: 1 actaactcaacgtcatt.....aaaaaaaaaaaaaaaaaaaaa 2198

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA Main:  
1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq.\*  
2: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq.\*  
3: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq.\*  
4: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq.\*  
5: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq.\*  
6: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq.\*  
7: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq.\*  
8: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq.\*  
9: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq.\*  
10: /cgn2\_6/ptodata/1/pubpna/US10F\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1284.8	58.5	2177	7	US-10-424-599-94124	Sequence 94124, A
2	664.8	30.2	2036	8	US-10-739-930-1070	Sequence 1070, Ap
3	657	29.9	1790	7	US-10-425-114-33374	Sequence 33374, A
4	657	29.9	1962	8	US-10-425-115-63646	Sequence 63646, A
5	561	25.5	1713	7	US-10-437-963-81205	Sequence 81205, A
6	327.4	14.9	1056	8	US-10-425-115-11856	Sequence 11856, A
7	273.6	12.4	887	7	US-10-437-963-81203	Sequence 81203, A
8	245.2	11.2	650	7	US-10-021-323-9030	Sequence 9030, Ap
9	244.8	11.1	853	8	US-10-425-115-63643	Sequence 63643, A
10	176.4	8.0	553	7	US-10-424-599-64336	Sequence 64336, A
11	145.8	6.6	567	7	US-10-021-323-7941	Sequence 7941, Ap
12	144	6.6	554	7	US-10-437-963-19720	Sequence 19720, A
13	110.8	5.0	812	8	US-10-425-115-63644	Sequence 63644, A
14	108.4	4.9	466	8	US-10-425-115-112285	Sequence 112285, A
15	86.8	3.9	860	8	US-10-425-115-172748	Sequence 172748, A
16	86.2	3.9	810	7	US-10-425-114-27910	Sequence 27910, A
17	84.2	3.8	287	3	US-09-294-0938-5780	Sequence 5780, Ap
18	75.4	3.4	279	7	US-10-424-599-24082	Sequence 24082, A
19	68.4	3.1	271	7	US-10-424-599-71566	Sequence 71566, A
20	61.2	2.8	236	7	US-10-424-599-3541	Sequence 3541, Ap
21	58.6	2.7	954	7	US-10-424-599-123113	Sequence 123113, A
22	50.6	2.3	1538	7	US-10-437-963-5998	Sequence 5998, Ap
23	50.2	2.3	509	7	US-10-424-599-63519	Sequence 63519, A

## ALIGNMENTS

RESULT 1  
US-10-424-599-94124  
; Sequence 94124, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 94124  
; LENGTH: 2177  
; TYPE: DNA  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_56005C.1  
US-10-424-599-94124

Query Match	58.5%	Score	1284.8;	DB	7;	Length	2177;
Best Local Similarity	83.5%	Pred. No.	0;				
Matches	1612;	Conservative	0;	Mismatches	277;	Indels	41;
Gaps	12;						
QY	101	TCTTTAAACAAGCACCCCATCGTGAATCGTGTCTATAACGCCAAAATTTTCCATTTCC	160				
Db	170	TCTTCCATCTTTTACCTTTTCATGATCGTCCATACGCCACCTATTTCATTCGG	229				
QY	161	CTTTTGATT-TTTAGTTTATTTTTCGGAATTCGGAGTTGGGGCGCAATTTGATGATGGT	219				
Db	230	TTTCCCTCTCTTTTCATTCGATCTTTTTCCTCTCTTTTCGCGCAATTTTTCGATGGGT	289				
QY	220	CTGTTGACGAATCTTCGAGGCTCGAGACAGATGGT-CCCAACAAGAGCACTTACCC	276				
Db	290	CTCGTGTGGAATCTCGAGGCTCGAGAACGGAAGTCCGCCACAACTAGAACCATTACCC	349				
QY	277	GTTC-----TGGCTCCGGAGGCAACCCAAAGAGGAATTCGAGCAATCTAATGCCTCTTGT	332				
Db	350	GTTCCTGCGGTTTCGAGTTCGCTCCGAGAGGAATTCGACCAATCTAATGCAAGCTGG	409				
QY	333	TGTTGCGCTT--GTGGTCAATCGCGAGA-TGCGTTTCTGGGTAGGTGGATATGCGCA	389				
Db	410	TGTCGCGCTAGTCTGTTGCGGAGAGTTCGCTTTCTCGGAGGCTCGACATGCGCA	469				



QY	1456	GAAGGTTTGAGATGAGTCCATTACCTGAGGCTTAGCAATTTAACTCTGAATGCTGTG	1515
DB	1550	GAAGGTTTGAGATGGAATCCATTACTTGAGTCTAGCAATTTAACTCTAGAGGCTTG	1609
QY	1516	AAGGCTGCTGTTGTTTGAAGTTACATCCCTGAAATCTTTGTCCTGTATGGAAGACTGAA	1575
DB	1610	AGTCTGCTGTTGTTTCAAGTTTCAATCCCTGAAATCATGTACCTATATGGAAGACAGAA	1669
QY	1576	AGGCTGAAGTTTAAAGAGGGGGAGTGTCTTTAAAACCTCTACAAATATATACCAATGGC	1635
DB	1670	AGACCTGAAATTTCTTAGAGGGGGCAATGATTTTAAAACTCTACAAATATATACCAATGGG	1729
QY	1636	TTGACACAGAGACAGCTCTTTATACCTTCAGCTTCAAAAGGTGATGCTGATTTACAGAGT	1695
DB	1730	TTGACACAAAGACAAAGCTCTTTATACCTTCAGCTTCAAAAGGGATGACATTTACAGAGT	1789
QY	1696	CACCTTGGAGAACATCTTGTGCAAGTTTGAAGTCATTTTGTGTAGCATGCGCTAAAT	1755
DB	1790	CACCTTGGAAAGCAATCTTGTGCAAGTTTGAAGTCATTTTGTGTAGCATGCT-AGT	1848
QY	1756	GGTACCTCTGCTACCTGAAAT--TAGCTTCACTTAGCTGAGCACTAGCTAGAGTTTAG	1813
DB	1849	GGCTCTCTGCTCTCATGAAATAGCTTTCTTCACTTAACTGAGC---GGTAGAGTTTAG	1904
QY	1814	GAATGATGATGAGTGAATATGAGTGGCTTTTATTTATGCTTGTGCTTCTTGGCCAACTC	1873
DB	1905	GGATGATGATGAGTGAATATGAGTGGCTTTTATTTATGCTTGTGCTTCTTGGCCAACTC	1964
QY	1874	ATTGATGTTTGTATGAAGACATCACACTTTTAAATTTTAACTTGTGTTCTGT-AGAAGTG	1930
DB	1965	ATTGATGATTTATTTTCAAAAGATAATCTTACTTTTGAACCTTTTGTGTACAAAGAGTG	2024
QY	1931	CAAAATCAATTTTAAATGCTTGTAGTTTAGT-----GCTCTTATCTGATCATCTAGAGTC	1984
DB	2025	AGGTTCCATATTTAAATGCTTGTAGTTTATGATATAGAGTTTCTATCTGATCATCTAGAAAG	2084
QY	1985	ACAGTTCTTG 1994	
DB	2085	CCACATGATG 2094	
RESULT 2			
US-10-739-930-1070			
; Sequence 1070, Application US/10739930			
; Publication No. US20040216190A1			
; GENERAL INFORMATION:			
; APPLICANT: Kovalic, David K.			
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH			
; TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT			
; FILE REFERENCES: 38-21(53377)B			
; CURRENT APPLICATION NUMBER: US/10/739,930			
; CURRENT FILING DATE: 2003-12-18			
; NUMBER OF SEQ ID NOS: 11088			
; SEQ ID NO 1070			
; LENGTH: 2036			
; TYPE: DNA			
; ORGANISM: Arabidopsis thaliana			
; FEATURE:			
; OTHER INFORMATION: Clone ID: ARATH-23APR03-CLUSTER5688_1			
US-10-739-930-1070			
Query Match 30.2%; Score 564.8; DB 8; Length 2036;			
Best Local Similarity 68.2%; Pred. No. 1.6e-172;			
Matches 989; Conservative 0; Mismatches 442; Indels 19; Gaps 4;			
QY	301	AAGAGGAAATGGAGCAATCTAAATGCTTCTTGTGTCCTTGTGTCCTTGTGTCATCCGAGATC	360
DB	268	AAGCAAAATATCGAATTTGTACCACTCTGCGTTGCTCTGGTAGTTATCGCTGAGATC	327
QY	361	CGCTTCTGGGTAGTTGGATATGGCCAAACCCCGCATGGTTGACTCCCTCGCTGAC	420
DB	328	GGGTTTCTGGTCCGCTCGAT-----AAAGTCGTTGGTTGATACGTTGACTGAT	378

QY	390	AAACGCCGCCATGTTGACTCCCTCGCTGACTTCTTACCGCTCTCGAGCGGTGTTGA	449
DB	470	GAACGCCGAGATGGTTGACACCTCGCTGCTTCTTACCGCCCTCGCGCAGTGGTTGA	529
QY	450	AGGTGACGATTTGGGGTTGGGTTTGGTGGCTT-----CTGATCGGAATCTG	496
DB	530	AGCGACGATTTGGGGCTGGGTAATATAGGTTGGTGGCGGGTTTCGGTGTGGAATCTA	589
QY	497	AATCGTATAGTTGTA-GGATGGTTGGAGGGGAGTGTCTGACGTATTCGAGGGC	555
DB	590	TTTCGATCGATGATGAGTGGTTGGAGAGGGAGTGCAGTGACTTATTCAGGGAC	649
QY	556	TTTTTCAAAAGAGCTATTTTGTCTTCTGGAGCTGATCAGGAGTGGAAAGTCGTGTTCCGGTT	615
DB	650	TTTGGCGAAGACCTGTTTGTCTTCTGGAGCTCTGATTGAATGGAAGTCATGCTCAGTG	709
QY	616	GGATGTAATTTGGGTTTATGTTGGGATAGAAAGCCAGATGCCGCATTTGGGTTACCTCA	675
DB	710	GGATGTAATTTGGGTTTATGTTGGGATAGAAACCTGATGCTGATTTGGGTTACCTCA	769
QY	676	CCAAGTGGACAGCTAGCATCTCTCGCATCAATGGAATCAGCAGAACTACTATGCTGAGAAC	735
DB	770	CCAGGTGAACAGCTAGCGTTCTCGCATCGATGGAATCAGCAGAACTACTATGCTGAGAAC	829
QY	736	AATATTGCCATGCGAAGCGAGGGGATATAACATCGTAAATGACAAACCAAGTCTATCTTCG	795
DB	830	AATCTTGCCATGCGAAGCGAGGGGATATGACATGTAATGACAAACCAAGTCTATCATCT	889
QY	796	GATGTTCTCTTGGATATTTTTCATGGCTGAGTATGATGATGATGAGCAGCTGCAGCGG	855
DB	890	GATGTTCTCTTGGATATTTTTCATGGCTGAGTATGACATCATGCGACCAATGAAGCCA	949
QY	856	AAACTGAACTGCTCTTGCAGCTGCTTTCATTTCCAAATGCTGCTCGAAATTTCCCGG	915
DB	950	AAAACTGAAGTCTCTTGCAGCTGCAATCATTTCCAAATGCTGCTCGAAATTTCCCGG	1009
QY	916	TTGCAAGCTCTTGAAGCCCTTGAATAATCAAAATCAAAATGGAATTTGATTTATGGTGGTTGT	975
DB	1010	TTGCAAGCTCTTGAAGCCCTTGAATAATCAAAATCAAAATGGAATTTGATTTATGGTGGTTGT	1069
QY	976	CACAGGAACCGTGAAGAGTGAAACAAAGTGAAGCCCTGGAAGCACTACAAATTTAGC	1035
DB	1070	CATAGGAACCGTGAAGAGTGGAATAAAGTGAAGCCCTTGAAGCACTACAAATTTAGC	1129
QY	1036	TTAGCTTGAATTTGAAATTCGAATGGAAGATTTATGTAATGAAATTTCTTCCAAATCCCTT	1095
DB	1130	TTAGCATTTGAAATTTCTAATGGAAGATTTATGTAATGAAATTTCTTCCAAATCCCTT	1189
QY	1096	GTTGCTGGAAGTCTCCCTGTTGTTGTTGCTCCAAATATTCAGGACTTTGCTCTTCT	1155
DB	1190	GTTGCTGGAAGTCTCCCTGTTGTTGTTGCTCCAAATATTCAGGACTTTGCTCTTCT	1249
QY	1156	CCTGGTTCAATTTTACATATTAAGAGATGAGATGTTGAGTCTGTTGGAAGACCATG	1215
DB	1250	CCTGGTTCAATTTTACATATTAAGAGATGAGATGTTGAGTCTGTTGGAAGTCCATG	1309
QY	1216	AGATATCTAGCAGAAATCCCGAAGCATATAATCAATCATTTGAGTGGAGTATGAGGT	1275
DB	1310	AGATACCTTAGCAGAAATCCCGAAGCATATAATCAATCTTTGAGTGGAGTATGAGGC	1369
QY	1276	CCATCTGACTCTTCAAGGCCCTTGTGGATATGGCAGCTGTGCAATTCATCGTCCGCTTT	1335
DB	1370	CCATCTGATCTTCAAGGCCCTTGTGGATATGGCAGCTGTGCAATTCATCGTCCGCTTT	1429
QY	1336	TGCATTCATTTGGCCACAGTGAAGAGAGAGAGAAATATTCAGGCTTAAAGAGA	1395
DB	1430	TGCATTCATTTGGCCACAGTGAAGAGAGAGAGAAATATTCAGGCTTCAACAAA	1489
QY	1396	CGTCTTGAAGTGCATAGAGGGCCAGAAACCGTATATCATATCATGTCAGAGAAAGG	1455
DB	1490	GGCCCTTGCAAGTGCATAGAGGGCCAAATACTGTGTATCATATTTATGAGAGAAAGG	1549

Qy	421	TTCTTCTVACCGCTCTCGAGCGGTGCTTTGAAAGGTGACGATTTGGGGTTGGGTTTGGTGGCT	480
Db	379	TTCTTCAACCAGTCTCGTCACTCTCGACTCTCCACCGCGAGATCCGATCGGAAGAAG	438
Qy	481	TCTGATCGGAATTTCTGAAATCGTATAGTTGTGAGGAATGGTTGGAGGGAGGAGTCTGTCT	540
Db	439	ATCGGATTTATTTACTGATAGG---AGCTCGAGAGTGGTTGATGAGAGAAGATTCAGTT	495
Qy	541	ACGTATTTTCGAGGGCTTTTCCAAAGAGCCTATTTTGTGTTTCTGGAGCTGATCAGGAGTGG	600
Db	496	ACTTACTCTAGAGATTTTACTAAAGATCCAAATTTTATCTCTGGTGGTGAAGAGACTTT	555
Qy	601	AAGTCGTGTTCCGTTGGATGTAAATTTGGGTTTAGTGGGGATTAAGAAGCCAGATCGCGCA	660
Db	556	CAATGGTGTCTGTGGATTCTACATTTGGAGATAGTTTCAGGGAAAAACACAGATGCTGCG	615
Qy	661	TTTGGGTTACTCAACCAAGTGAACAGCTAGCATCTCTGCATCAATGGAATCAGACAGAA	720
Db	616	TTTGGATTAGGTGAGAAACCTGGAACTCTTAGTATTAATACGTTCCATGGAAATCAGACAG	675
Qy	721	TACTATGCTCGAGAACAAATATTGGCATGGCAAGACGGAGG---GGATATTAACATCGTAAT	776
Db	676	TATTATCCAGAAATGATCTTGCACAGCACGCGTGGAGAGGTTATGATATAGTGAT	735
Qy	777	GACAAACAGTCTATCTTTCGGATGTTCTGTGTGGATATTTTTCATGGGCTGAGTATGATAT	836
Db	736	GACCACTAGTCTATCATCAGATGTTCTGTGTGGATATTTTTCGTGGCGGAGTATGATAT	795
Qy	837	GATGGCACCACTGCAGCGGAACACTGAAGCTGCTCTGTGCAGCTGCTTCAATTTCCAAATTC	896
Db	796	TATGTCTCCGGTACAGCCAAACACTGAGAGAGCTATTTCGAGCTGCTTTTATTTCTTAATTC	855
Qy	897	TGTTGCTTCGAAATTTTCCGGTTGCAAGCTCTTGAGGCCCTTTCAAAAAATCAAAACATCAAAAT	956
Db	856	TGTTGCTCGGAATTTTCGTCTACAGACACTTGAGGCATTCGATGAAACTTAACATTAAAT	915
Qy	957	TGATTTCTTATGGTGGTTGTACAGAGAACCGTGATGGAAGAGTGAAACAAAGTGGAAGCCCT	1016
Db	916	TGATTTCTTATGGTGGTTGTATCGAACCAGGATGGGAAAGTTTGACAAGGTTGAAAGCTCT	975
Qy	1017	GAAGCACTACAAATTTAGCTTTAGCGTTTGAAATTTCCAAATGAGGAGATTTATGTACTGA	1076
Db	976	TAAAGCGATACAAATTTAGTTTGGCTTTTGAGAAATCTAACAGGAAGATTTATGTACCGGA	1035
Qy	1077	AAAATTTCTTCAATCCCTGTTGCTGGAACTGTCCCTGTGGTTGTTGGTGCCTCCAAATAT	1136
Db	1036	GAAGTTCTTTCAATCTCTAGTTGCTGGGTCCGTCCCGCTGGTAGTTGCTCTCCAAATAT	1095
Qy	1137	TCAGGACTTTGCTCTCTCTCTGTTCCAAATTTTACATATTAAGAGATAGAGGATGTTGA	1196
Db	1096	AGAAGATTTTGGCGCTGCTTCGGACTCATTTCTTCAATTTAAAGACTATGGAAGATGTAGA	1155
Qy	1197	GTCTGTTGCAAGACATGAGATATCTAGCAGAAAAATCCCGAAGCATATTAATCAATCATTT	1256
Db	1156	GCCAGTTGCAAGAGAAATGAAGTATCTCGCAGCTTAACCTCTGCTCTTATTAATCAGACACT	1215
Qy	1257	GAGGTGAAGTATGAGGGTCCATCTGACTCTCTTCAAGGCCCTTGTGGATATGGCAGCTGT	1316
Db	1216	AAGATGAANAATCGAGGGTCTCTCAGATTTCTTTCAAGGCACTTGTTGATATGGCTGCTGT	1275
Qy	1317	GCATTTCACTGTCGCGCTCTTTTGCATTTCACTTGGCCACAGTGAAGTGAAGAGGAAGAAA	1376
Db	1276	ACACTCTTCTTGGCGTCTCTGCATTTTCTTGGCCACGAGGCTCCGAGAACAAAGAAGAGGA	1335
Qy	1377	TAAATCCAAGCGTTAAGAGACGTCTCTTGCAGT---GCACCTAGAGGCCAGAAACCGTATA	1433
Db	1336	AAGCCCTAAATTTCAAGAAAAACGACCGTGCAAATGTAGCAGGGGAGGATCAGACACAGTTTA	1395
Qy	1434	TCATATCTATGTTCAGAGAAAGGGGAAGGTTTGACATGGAGTCCATTTTACCTGAGTCTAG	1493
Db	1396	TCATGTTTTTTGTAGAGAAAGAGCCCGTTTTGAAATGGAATCAGTCTTTTTTGGGGGTAA	1455
Qy	1494	CAATTTAACTCTGAAATGCTGTGAAGGGCTGCTGTTGTTTGAAGTTACATCCCTCGAATCT	1553

```

1456 AAGTGTGACTCAGGAAGCTCTAGAATCTCGAGTTCTGCCAAGTTCAGTCTTTAAACA 1513
1554 TGTGCCCTGTATGGAAGACTGAAGAGGCTCGAAGTTATAAGAGGGGGAGTGTCTTTAAACT 1613
1516 TGAGGCAGTGTGGAAGAAGGAAAGGCTCGAAACTTTAAAGGAGACAAAAGAGCTTAAAT 1575
1614 CTCAAAATATACCCCAATTGGCTTGCACACAGACACAAGCTCTTTATACCTTTCAGCTTCAA 1673
1576 ACATCGGAATTTACCCGCTTGGCTTAACGCAACGACAGGCTTTGTATCAACTTCAAAATTCGA 1635
1674 AGGTGATGCTGATTTTCAGGAGTCACTTGGAGAAACAATTCCTTGTGCCAAGTTTGAAGTCAT 1733
1636 GCGAAATTCGAGTCTAAGTAGTCACATTCAAAACAACCCCTTGTGCTAAATTTGAGGTGT 1695
1734 TTTTGTGCTAG 1743
1696 CTTGCTGCTAG 1705

RESULT 3
US-10-425-114-33374
; Sequence 33374, Application US/10425114
; Publication No. US20040034898A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovacic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 33374
; LENGTH: 1790
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLMO17102G04_FLI
US-10-425-114-33374

```

Query Match	29.9%	Score 657;	DB 7;	Length 1790;
Best Local Similarity	56.3%;	Pred. No. 2.1e-170;		
Matches	964;	Conservative 0;	Mismatches 480;	Indels 9; Gaps 1;
Qy	301	AAGGGAATGGAGCAATCTAATGCCTCTGTGTGTGTGCGCCCTTGTGCTCATCGCGGAGATC	360	
Db	166	AGGCGGCGCTGGGGGTGCTTCTGCGCGCTCCTCGTTGGCGCCGCTTCTTCGCGGAGATC	225	
Qy	361	CGCTTTCTCGGTAGTTGGATATGGCCAAACCGCCGCCATGTTGTGACTCCCTCGCTGAC	420	
Db	226	CGCTTCTCGCGCGCTCGACATGGCGAAGAACGCCGAGCGGTTCGAGAGCTGGACCACC	285	
Qy	421	TTCTTTTACCGCTCTCGAGCGGTCTGTGAAGGTGACGATTTGGGGTTGGGTTTGGTGGCT	480	
Db	286	TCCTTTTACCGCGCTCCGCGGATTTGGCGGATGCGCTTGGCGGGGCGCAGACCTCGAGG	345	
Qy	481	TCTGATCGGAATTCTGNAATCGTATGT- - - - -TGTCAGGAATGTGTTGGAGAGGGAG	531	
Db	346	GCAGGCGGCGACAGCGAGGACGAGAGATCCGGCTGTGCGAGCAGCGGCTCGAGAGGGAG	405	
Qy	532	GATGCTCTCACGTATTTCAGGGGGCTTTTCCAAAGAGCCTATTTTGTGTTTCTGAGGCTGAT	591	
Db	406	GATGCCGTGCCCTACGACCGGCACTTTTGACAGTGATCCCGTGTGTTGCGGTGGCGCTGCC	465	
Qy	592	CAGGAGTGGAGTCGTGTTTCGGTTTGGATGTAAATTTGGGTTTGTAGTGGGATAGAAAGCCA	651	
Db	466	AAGGATTTGGAAATAATGCTACGTAGGATGTGAATTTGGTTTCTTCGCGAGTAGACACCT	525	

Qy	652	GATGCCGCAATTTGGGTTACTCAACCAGATGGAAACAGCTAGCATTTCTGCGATCAATGGAA	711
Db	526	GATGCTACATTTTGGAAATTTGCAACAGATCCTTCTGTAGATGGTATCTCTCAGATCAATGGAA	585
Qy	712	TCAGCAGAAATACATCTCTCAGAAACAATATTTGCCATGGCAAGACGGAGGGGATATACATC	771
Db	586	TCATCTCAATATATTTACAGAAATAATATTTGATGTGGCTCGAGGGAGAGGGTACAGGATT	645
Qy	772	GTAATGACAACAGTCTATCTTCGGATGTTCTGTTGGATATTTTTTCATGGGCTCAGAT	831
Db	646	GTGATGACAAACAGCCCTTCTTCAGACGACACAGATTTGGCTACTTTTTCATGGGCTGAATAT	705
Qy	832	GATATGATGCAACAGTCAGCGCGAAATATGAAGCTGCTCTTGCAGCTCCTTTTCATTTCC	891
Db	706	GATATCATGGCACTGTGCTCCAAAGACTGAAGAGCTTGTCTGCAGCCCTTTATTTCT	765
Qy	892	AAATGTGTGCTCGAAATTTCCGGTTGCAAGCTCTTGGGCCCTTTGAAAAATCAACATC	951
Db	766	AACGTGTGCACGAACTTTCTGTTTGAAGCCCTTGAGATGTTGAAAACTTTGGATGTC	825
Qy	952	AAAATTTGATTTTATGTTGTTGTCACAGAAACCGTGATGGAGAGTGAGCAAAAGTGGAA	1011
Db	826	AAAATGATTTCATATGTTAGTTGTCTATCGTTTGAAGCCCTTGAGATGTTGAAAACTTTGGATGTC	885
Qy	1012	GCCTGGAAGCACTACAAATTTAGCTTAGCCCTTTGAAAAATTCGAATCAGGAAGATTATGTA	1071
Db	886	ACTTTGAAGCGCTACAGATTCAGCTTGGCATTTGAGNAATTCATCAGGAGGATTATGTA	945
Qy	1072	ACTGAAAAATTTCTTCCAATCCCTTGTGTGTGGAACGTGTCCTGTGTGTTGTTGTGTCCTCA	1131
Db	946	ACTGAAAGTTTTTTTTCAGTCACTAGTAGCAGGTTCTATTCCGGTTGTTGTGTGTCCTCA	1005
Qy	1132	AAATTTCAGGACTTTGCTCCTTCTCTCGTTTCAATTTTACATATTAAGAGAGATAGAGGAT	1191
Db	1006	AAATATCAAGAGTTTCTTCGCGGAGAGGGCGCAATATTTACATATTAAGGAGCTTGATAT	1065
Qy	1192	GTTTCAGTCTGTGCAAGACCATCAGATATCTAGCAGAAAAATCCGGAAGCATATAATCAA	1251
Db	1066	GTTGCTTCAGTTGTAGACAAATGAAATATTTGCTTCAAACTGATGCTTCAATCAA	1125
Qy	1252	TCATGTAGGTGGAATGATGAGGTTCATCTGACCTCTTCAAGGCCCTTGTGGATATGGCA	1311
Db	1126	TCTTTAGGTGGAATGATGATGTTCCATCCGATTTCTTTCAAAGCTCTTATTTGACATGGCA	1185
Qy	1312	CTGTGCAATTCATCGTCCGCTTTTGATTTTGCATTCACCTTGCCCAAGTGACTAGAGAGAAGAA	1371
Db	1186	CGGTTCAATTCATCTGTGCTGTTGTATATCATATGCTACCAAGATCCATTTAAAGGAG	1245
Qy	1372	GAAATAATCCAAGCCTTAAAGACGCTCTTGCAAGTGCATAGAGGGCCAGAAACCGTA	1431
Db	1246	GAAAGGACTCCAAAATTTTACAAATTCGCTCTTGTAGCTTCCACCAAAAAGGGAACAAT	1305
Qy	1432	TATCATATCTATGTACAGAAAGGGGAAGTTTGAGATGGAGTCCATTTACCTGAGTCT	1491
Db	1306	TACCACCTTATTTATCCGAGAGAGAGGGGGTTAAGTCAGAGAGCATTTTACATGAGATCA	1365
Qy	1492	AGCAATTTAACTCTGAATGCTGTGNAAGCTGCTGTTGTTTGAAGTTTCACATCCCTCAAT	1551
Db	1366	GGCCAGTTAACTCTGGGAGCCTTGGAAATCCGAGTGCTCGGTAAATTTAGTCCCTCAAC	1425
Qy	1552	CTTGTGCTGTATGGAAGACTGAAAGCCCTGAAGTTATAGAGGGGGGAGTGCTTTAAAA	1611
Db	1426	CAGGTTCTGTATGGAAGATGAAGGCCACCGAGCATTAGAGGTGGGATGACCTGAAA	1485
Qy	1612	CTCTCAAAAATATACCAATTTGGCTTTGACACAGAGACAAGCTCTTTATACCTTCAGCTTC	1671
Db	1486	TTATACAGAAATTTACCCAGTCGCTTAAACGCAACGCTCAGGCTTTGTACGGTTTTAGATT	1545
Qy	1672	AAAGGTGATGCTGATTTTACGAGAGTCACTTTGGAGAACAACTCTTTGTGCCAAGTTTGAAGTC	1731
Db	1546	AGGGATGATTTCTGAACTCGAGCAATATATCAAGACCACTCTCTGTGCAAGCTTGAAGTA	1605
Qy	1732	ATTTTGTGTAGC	1744

```

|||||
Db      1606 ATTTTGTGAAC 1618

RESULT 4
US-10-425-115-63646
; Sequence 63646, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 63646
; LENGTH: 1962
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MFT4577_158045C.1
US-10-425-115-63646

```

Query Match	29.9%;	Score 657;	DB 8;	Length 1962;
Best Local Similarity	66.3%;	Prim. No. 2.2e-170;		
Matches 964;	Conservative	0;	Mismatches 480;	Indels 9; Gaps 1;
QY	301	AAGAGGAATCGAGCAATCTAATGCCTCTGTTGTTGGCCCTTGTGGTTCATCGCGAGATC	360	
DB	301	AGGCGGCCCTGGGGTGTTCTTCGCCGTCTCTCGTTGGCGGCCCTTCTCGCCGAGATC	360	
QY	361	GGTTTTCTGGGTAGGTTTCGATATATGGCCAAAAACCGCCCATAGTTGATCCCTCGCTGAC	420	
DB	361	GGTTTCTCGCGCCCTCGACATGGCGAAGAACGCGAGGCGGTCTCGAGAGCTGGACACC	420	
QY	421	TTCTTCTACCGCTCTCGAGCGGTGCTTGAAGTGACGAATTTGGGGTTGGGTTTGGTGGCT	480	
DB	421	TCCTTTTACCGCGCTCCGCGGATTTGGCGGATCGCGTTGGCGGGGCGACGCTCGAG	480	
QY	481	TCGTATCGGAATTCCTGAATCGTATAGT-----TGTGAGGAATGGTTGGAGGGGAG	531	
DB	481	GACGGCGGACAGCGAGGACGAGAGATCCGGCTGTCGACAGCGGCTCGAGAGGGAG	540	
QY	532	GATGCTGTCACTAATTCGAGGGGCTTTTCCAAAGAGCCCTAATTTGTTGTTCTGGAGCTGAT	591	
DB	541	GATGCGTGCCTTACGACCGGACCTTGACAGTGATCCCGTGCTTGTCTGGTGGCGTGCC	600	
QY	592	CAGGAGTGAAGTCTGTTTCGGTTGGATGTAATTTGGTTTGTAGTGGGATAGAAAGCCA	651	
DB	601	AAGGATTGAATAAATGCTACGTAGGATGTGAATTTGGTTTTTCTGCGAGTAGACACCT	660	
QY	652	GATGCGGCAATTTGGGTACTCTCAACAGTGGAAACAGCTAGCAATCTCGCATCAATGGAA	711	
DB	661	GATGTACATTTGGGAATTCGACAGATCCCTCTGTAGATGGTATCCTCAGATCAATGGAA	720	
QY	712	TCAGCAGAATCTATGCTCAGAACAAATATTGCCATGCGAAGACGAGGGGATATAATC	771	
DB	721	TCATCTCAATATTATTCAGAGAAATAATTGATGTGGCTCGAGGGAGAGGGTACAAGATT	780	
QY	772	GTAATGACAAACAGTCTATCTTCGGAATGTTCTGTGGTATATTTTTCATGGGCTGAGTAT	831	
DB	781	GTGATGACAAACAGCCCTTCTTCAGACGTAACAATTTGGCTACTTTTTCATGGGCTGAATAT	840	
QY	832	GATATGATGGCACCAGTGCAGCCGAAACCTGGAAGCTCTTCGAGCTGCTTTCAATTC	891	
DB	841	GATATCATGGCACCTGTGGCTCCAAAGACTGGAAGAGCTCTTGCTGCAGCCTTTATTTCT	900	
QY	892	AATTGTGGTGTCTCGAAATTTCCGGTTGCAAGCTCTTTGAGGCCCTTTGAAAAATCAACATC	951	



[illegible]

RESULT 6

US-10-425-115-11856

; Sequence 11856, Application US/10425115

; Publication No. US200402114272A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

; TITLE OF INVENTION: Plants

; FILE REFERENCE: 38-21(53222)B

; CURRENT APPLICATION NUMBER: US/10/425,115

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 369326

; SEQ ID NO 11856

; LENGTH: 1056

; TYPE: DNA

; ORGANISM: Zea mays

; FEATURE:

; OTHER INFORMATION: Clone ID: MRT4577\_11080C.1

US-10-425-115-11856

	Query Match	14.9%;	Score 327.4;	DB 8;	Length 1056;
	Best Local Similarity	74.5%;	Pred. No. 2.8e-79;		
	Matches 412;	Conservative	0;	Mismatches 141;	Indels 0; Gaps 0;
QY	709	GAATCAGCAGAGATACTATGCTGAGACAAATATTGCCATGCGAAGACGGAGGGGATATAAC	768		
DB	413	GAACCAATGTTCTATTGGTCTGGCAATTTCAITGCTTTCTATAACAGGAGAGGGGTACAAG	472		
QY	769	ATCGTAAATGACACACAGTCTACTTCGGATGTTTCGTGTGGATATATTTTCATGGGCTGAG	828		
DB	473	ATTGTGATGACAAACAGCCTTTCTTCAGACGTACCAAGTTGGCTACTTTTCATGGGCTGAA	532		
QY	829	TATGATATGATGSCACAGTCAGCGCCGAAAACTGAAGCTGCTCTTGACGCTGCTTTTCATT	898		
DB	533	TATGATATCATGGCACCTGTGCTCTCAAAAGACTGAAAGAACTCTTGCTGCAGCTTTATT	592		
QY	889	TCCAAATGTGGTCTGGAATTTCCGTTGTCGAAGCTCTTGAGGCCCTTGAAAAATCAAAAC	948		
DB	593	TCTAACTGTGGTGCAAGAACTTTGTTTGAAGCCCTTGAGATGCTTGAANAATTGGAT	652		
QY	949	ATCAAAATTGATTCTTTATGGTGGTGTGTCACAGGAAACGGTGATGGAAGAGTGAACAAAGTG	1008		

Db	653	GTCAAAATAGATTTCATATGTTAGTTGTTCATCTGTAACCGGTGACGGCAAAAGTGCACAAAGTG	712
Qy	1009	GAAGCCCTCAGCAGCTACAAATTTAGCTTAGCGTTTGAAAAATTCGAATCAGGAAGATTAT	1068
Db	713	GACACTTTGAAGCGCTACAGATTACGCTTGGCATTTGAGAAATCTAATGAGGAGGATTAT	772
Qy	1069	GTAACCTGAAAAATTCCTCCAAATCCCTGTTGCTGGAACCTGTCCTCTGTGCTGTGCTGCT	1128
Db	773	GTAACCTGAAAAGTTTTCCTCAGTCACATGACAGAGGTTCTATTCCCGTTGTTGTTGCTGCT	832
Qy	1129	CCAAATATTTCAGGACTTTTCTCTCTCTGTTTCAATTTTACATATTAAAGAGATAGAG	1188
Db	833	CCAAATATTTCAGAGTTTCTCCGGGAGAGGCGCAATATACATATTAAAGGAGCTTGAT	892
Qy	1189	GATGTTGAGTCTGTGTCAAAGACCAATGAGATATCTAGCAGAAAAATCCCGAAGCATATAT	1248
Db	893	GATGTTGCTTCAGTTCTGAAGCAATGAAAAATATTGCTTCAAACCTGATGCTTCAAT	952
Qy	1249	CAATCATTTGAGGT	1261
Db	953	CAATCTTTGAGGT	965

RESULT 7

US-10-437-963-81203

Sequence 81203, Application US/10437963

Publication No. US20040123343A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Kovalic, David K.

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

APPLICANT: Wu, Wei

APPLICANT: Boukharov, Andrey A.

APPLICANT: Barbazuk, Brad

APPLICANT: Li, Ping

TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with Rice

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53221)B

CURRENT APPLICATION NUMBER: US/10/437,963

CURRENT FILING DATE: 2003-05-14

NUMBER OF SEQ ID NOS: 204966

SEQ ID NO 81203

LENGTH: 887

TYPE: DNA

ORGANISM: Oryza sativa

FEATURE:

OTHER INFORMATION: Clone ID: PAT\_MRT4530\_80753C.1

US-10-437-963-81203

Query Match	12.4%	Score 273.6	DB 7	Length 887
Best Local Similarity	66.0%	Pred. No. 2e-64		
Matches 396	Conservative 0	Mismatches 204	Indels 0	Gaps 0
QY	432	CTCTCGACCGTCGTTGAGGTGACGATTCGGGGTTGGGTTTGGTGGCTTCTGATCGGAA	491	
Db	288	CCCGGCGCGACCGGACGACGGCCCCCGCGGAGGTGAGTGGTGGAGGAGGACGA	347	
QY	492	TTCTCGAATCGTATAGTTTCTGAGGAATGTTTGGAGAGGAGGAGTGTGTTCAGCTATTCGAG	551	
Db	348	CGGCGACATCCGTTGTGCGAGGAGCGGCTTTGAGAGGAGGACGGCGTGCCTCCACGACCG	407	
QY	552	GGGCTTTTCCAAAGAGCCCTATTTTTTGTGAGAGCTCATCAGGAGTCGAGTCTGGTTC	611	
Db	408	CGACTTCGACAGGATCCGCTCTCGTCGGGGGCGCCCTAAGGAATTGGAATPAATGTTTC	467	
QY	612	GTTTCGATGTAATTTTGGTTTTAGTGGGATAGAAAGCCAGATGCCGATTTGGGTACC	671	
Db	468	TGTAGGATGTGAATTTGGTTTTTTCAGCTACTAAGACGCGCTGATGCTACTTTTGGAAATTCG	527	
QY	672	TCAACCAAGTGGAAACAGCTAGCATTTCTCGATTCAAATGGAATCAGCAGAAATACATGCTGA	731	





Qy	1777	TTAGCTTCATTAGCTGAGCACTAGCTAGAGTATTTAGGAATGAGTATGCGCAGTGAATATG	1836
Db	313	AAAAGCTTTTCCCTTAACTGACCGGGAAGTTTTAGGGATGAGTATGGCCATGAAACTG	254
Qy	1837	GCATGCCTTATTATGCCCTAGTCTTCTGGCCAACTCAATTGATGTTTCTATATAAGACATC	1896
Db	253	GCGGGCTTTTATTATGCAAGAGCTTTTGGCCCCCTTGGATGATTATATATTCCAAAA	194
Qy	1897	ACACTTTAATTTTAAACTTGTCTCTG - -- TAGAAGTGCAAAATCCCATTTAAATGCTTAGT	1953
Db	193	AAATTTTCCTTTTGAACCTCTTTTGGGCCAAAAGGGGGGCTTCCCCATTTAAAGCTTAGT	134
Qy	1954	TTTAGT	1959
Db	133	TTTAGT	128

```

RESULT 11
US-10-021-323-7941/c
; Sequence 7941, Application US/10021323
; Publication No. US20040123340A1
; GENERAL INFORMATION:
; APPLICANT: Deikman, Jill
; APPLICANT: Feng, Paul C.C.
; APPLICANT: Fincher, Karen L.
; APPLICANT: Ziegler, Todd E.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated Wi
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(52274)B
; CURRENT APPLICATION NUMBER: US/10/021,323
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 60/255, 619
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 17880
; SEQ ID NO 7941
; LENGTH: 567
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3828-022-Q1-N6-F4
US-10-021-323-7941

```

Query Match	6.6%;	Score 145.8;	DB 7;	Length 567;
Best Local Similarity	69.5%;	Pred. No. 3.8e-29;		
Matches 212;	Conservative 0;	Mismatches 92;	Indels 1;	Gaps 1;
1439	TCTATGTCAGAGAAAGGGAGGTTTCAGAGATGGAGTCCATTTACCTCAGGTT-CTAGCAAT	1497		
Db	566	TATACGTACGAGAACGAGGGAGGTTTATAGATGGATTCTATTTTTTAAAGTCCCGGGAA	507	
1498	TTAACTCTGAATGCTGTGAAGGCTGCTGTTGTTTTGAAGTTCACATCCCTCGAATCTTCGTG	1555		
Db	506	ATGACCTTTAAAGGGCTTTGGAGGCTGCCGTTCCACACGATTTTCAAGTTTCGGAAACACGTT	447	
1558	CCTGTATCGGAAGACTGAAAGGCCCTGAACTTTATAAGAGGGGGAGTGCCTTTAAACCTTCAC	1611		
Db	446	CCTATTTGGAAACCGGAAGAAGCCAGAAAGCCCTTCGAGGTGGAGATGAACCTAAAGATATAC	387	
1618	AAATATATACCAATTTGGCTTGACACAGAGACAAGGCTCTTTATATACCTTCAGCTTCAAGGT	1677		
Db	386	AGAAATATATCTCTCTTTGGGTTGCACACAAAGACAGGCTTTATATACATTCGAAGTTCAAAGG	327	
1678	GATGCTGATTTTCAGAGTTCACCTTGAGAGACAATCCCTGTCGCAAGTTTTGAAGTCATTTTT	1733		
Db	326	GATGCTGATCTTTAAGAACCATATCGAAAAACACCCTTGGCGAAGTTCGAAGTCATATTC	267	
1738	GTGTA	1742		
Db	266	GTGTA	262	

RESULT 12  
US-10-437-963-19720/c

QY	708	GGAAATCAGCAGAAATACTATGCTTGAGAAACAATATTGCCATGGCAACGACGAGGGGATATAA	767
DB	512	GGAAATCATCTCAATATTATTACAGAAATAAATATTGATGGCTCGAGGGTA-----	562
QY	768	CATCGTAANTGACNAACAGTCTATCTTCGATGCTTCGTGTGGATATTTTTCATGGGCTGA	827
DB	563	-----GATGTCACAGTTGGCTACTTTTCATGGGCTGA	594
QY	828	GTATGATATGATGGCACCACTAGTCAGCCGAAAACTGAAGCTGCTCTTGACAGCTGCTTTTCAT	887
DB	595	ATATGATATCATGGCACCTGTGCTCCAAAGACTGAAGAAGCTCTTGCTGTAGCCCTTTAT	654
QY	888	TTCCAAATGTGGTGCTCGAAATTTCCGGTTGCAAGCTCTTGAGGCCCTTGAAAAATCAAA	947
DB	655	TTCTAACTGTGGTGCACGGAACCTCCGTTTGCAGGCCCTTGAGATGCTTTNGAAATTTTGA	714
QY	948	CATCAAAATGATTTCTTATGTGTGTCACAGGAACCGTGATGGAAGAGTGAAACAAAGT	1007
DB	715	TGTCAAAANTAGATTCAATATGTTGTTGTCATCGTAACCGTGATGGCAAAGTGGACAAAGT	774
QY	1008	GGAAAGCCCTGAAGCACTACAAAATTAGCTTTAGCGTTTGAAAAATTCGAATGAGGAAATTA	1067
DB	775	GGACACCTTGAAGGCTACAGATTACAGCTGGGCAATTGAGAANTTCTATGAGGAGGATA	834
QY	1068	TGTAACCTGAAAAATTCCTT	1085
DB	835	CGTAACAGAAAAAGTTTTT	852

RESULT 10  
 US-10-424-599-64336/c  
 ; Sequence 64336, Application US/10424599  
 ; Publication No. US20040031072A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: La Rosa Thomas J  
 ; APPLICANT: Kovalic David K  
 ; APPLICANT: Zhou Yihua  
 ; APPLICANT: Cao Yongwei  
 ; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
 ; FILE REFERENCE: 38-21(53223)B  
 ; CURRENT APPLICATION NUMBER: US/10/424,599  
 ; CURRENT FILING DATE: 2003-04-28  
 ; NUMBER OF SEQ ID NOS: 285684  
 ; SEQ ID NO 64336  
 ; LENGTH: 553  
 ; TYPE: DNA  
 ; ORGANISM: Glycine max  
 ; FEATURE:  
 ; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_29107C.1  
 ; US-10-424-599-64336

	Query Match	8.0%;	Score 176.4;	DB 7;	Length 553;
	Best Local Similarity	66.7%;	Pred. No. 1.2e-37;		
	Matches 284;	Conservative	0;	Mismatches 136;	Indels 6; Gaps 2;
QY	1537	TTCCATCCCTGMACTCTTGTCCTGTATGGAAGACTGAAGGCCCTGAAGCTTATAAGAGGG	1596		
DB	550	TCGCCACCCCGAATCCAGGCCCCMAAGGGAAGCCAAAGCCCTCAANTTTAAAGGG	491		
QY	1597	GGGAGTGCCTTTAAAACTCTCAAAATATATACCAATTTGGCTTTGACACAGACAAAGCTCTT	1656		
DB	490	GGCCATGATTTAAAAACCCCCCAATAATAAACCCGGTGGGTGACCCAAAACCAAGCTTTT	431		
QY	1657	TATACCTTCAGCTTCAAAGGTGATGCTGATTTCAAGGAGTCACTTGGAGAACAACTCTTGT	1716		
DB	430	TAAACCTTTCCGCTTCCAAAGGGAGGCCGATTTTCAGGGGTCCCTTGGAAACCCCCCTTGG	371		
QY	1717	GCCAAAGTTGAAGTCAATTTTGTGTAGCATCGCTTAAATGGTATCCTCTGTCTTACCTGAA	1776		
DB	370	GTAAAGTTTGAATCAATTTTGTGTAGCATCGGC---AAGGGGCCCTCTCTCTCCCAAG	314		



; Sequence 19720, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 19720  
; LENGTH: 554  
; TYPE: DNA  
; ORGANISM: Oryza sativa  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_25153C.1  
US-10-437-963-19720

Query Match	6.6%;	Score 144;	DB 7;	Length 554;
Best Local Similarity	73.8%;	Pred. No. 1.2e-28;		
Matches 183;	Conservative 0;	Mismatches 65;	Indels 0;	Gaps 0;
QY	750	AAGACGGAGGGATATAACATCGTAATGACACCAAGCTCTATCTTCGGATGTTCTCTGTGG	809	
DB	537	AAACAGGAGAGGGTACAAGATTGTGATGACACTAGCCCTTCTTCAGATGTGCGAGTTGG	478	
QY	810	ATATTTTTCATGGGCTGAGTATGATGATGATGACACCAAGTGCAGCCGAAACTGAAAGCTGC	869	
DB	477	CTACTTTTCATGGGCTGATATGATATCATGACACTGTGCCTCCAAAGACTGAAAGC	418	
QY	870	TCTTGCAGCTGCTTTCAITTCCAATTTGGTGGTCTCGAAATTTCCGGTTGCAAGCTCTTGA	929	
DB	417	TCTTGTGCGAGCCTTTATTTTCAAGCTGTGGTGCACGAACTTCCGGTTTGCAGCCCTTGT	358	
QY	930	GGCCCTTGAANAATCAACATCAAAATTCATTTCTTATGGTGGTGTGTCAGGAAACCGTGA	989	
DB	357	GATGCTTGACCATTTGAAATGTCTACATAGATTTCATATGGTAGTGGTCATGGTAGCCGTGA	298	
QY	990	TGGAAGAG	997	
DB	297	TGTCAAAG	290	

RESULT 13  
US-10-425-115-63644  
; Sequence 63644, Application US/10425115  
; Publication No. US20040214272A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
; TITLE OF INVENTION: Plants  
; FILE REFERENCE: 38-21(53222)B  
; CURRENT APPLICATION NUMBER: US/10/425,115  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 369326  
; SEQ ID NO 63644  
; LENGTH: 812  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(812)  
; OTHER INFORMATION: unsure at all n locations



1852 TGCCTAGTTCCTGGCCAACTCATTGATGTTTGTATAAGACATCACACTTTAATTAA 1911

Db 883 TRVTCGCTTADYGTCTAAATMAAATTTTTTAAAAACAMGSCCAABGTMGTGTMGTGTTT 824  
 Qy 1912 ACTGTTTCTGAGAGTGAATCCATATTTTAAATGCTTAAAGTTTCTGCTTCTGTA 1971  
 Db 823 GAGATKYTGAAATTAATGASAAATATYATTTCAKRAATGCATTAAAGCTTWTBTYTTG 764  
 Qy 1972 TCATCTAGAAGTCACAGTCTCTGTATATTTGAGTGAAGAACTGAAATCTAATAGAAGAT 2031  
 Db 763 YGACAGTTANGCMAATVAGCTTGAATCCATATGTTCTCCTGASATATTTTATCMCAAGC 704  
 Qy 2032 CAGATGTTTCACTCAAGACATATTAATCTATCTGTTGTTTATGATGATCTCGAGCTTTT 2091  
 Db 703 CMCAHGTYGTTTATAAGSCASATVGYWATWATATATATAATCTCGAATCATGAACATGY 644  
 Qy 2092 TAGTGTCTGGAAGTCCCTGCTGTTGAGCAGCTGTTATGCTTCAAGTGTACTGTCCA 2151  
 Db 643 TCASYSATYTTCCYCCCTTGGATTGAAAAHWAATKHTATYTGKMCATTWAAATGGC 584  
 Qy 2152 GTGCTTATCTGTTTGGACCTCAAAAAAATTTTTTTTTTTTTTTTTTTTTT 2194  
 Db 583 AAAATWKGGTATYKATTWMSMTMAAAAAAARWMAWAVHGAA 541

RESULT 2

US-11-128-061-736  
 ; Sequence 736, Application US/11128061  
 ; Publication No. US20060003958A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Melville, Mark W.  
 ; APPLICANT: Charlebois, Timothy S.  
 ; APPLICANT: Mounts, William M.  
 ; APPLICANT: Hann, Louane E.  
 ; APPLICANT: Sinacore, Martin S.  
 ; APPLICANT: Leonard, Mark W.  
 ; APPLICANT: Miller, Christopher P.  
 ; APPLICANT: Brown, Eugene L.  
 ; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES RELATED TO OLIGONUCLEOTIDE ARRAYS  
 ; TITLE OF INVENTION: TO MONITOR GENE EXPRESSION  
 ; FILE REFERENCE: 01997.027701  
 ; CURRENT APPLICATION NUMBER: US/11/128,061  
 ; CURRENT FILING DATE: 2005-05-11  
 ; PRIOR APPLICATION NUMBER: US 60/570,425  
 ; PRIOR FILING DATE: 2004-05-11  
 ; NUMBER OF SEQ ID NOS: 7285  
 ; SOFTWARE: PatentIn version 3.3  
 ; SEQ ID NO 736  
 ; LENGTH: 1705  
 ; TYPE: DNA  
 ; ORGANISM: Cricetulus griseus  
 ; FEATURE:  
 ; NAME/KEY: misc\_feature  
 ; LOCATION: (1505)..(1521)  
 ; OTHER INFORMATION: n is a, c, g, or t  
 US-11-128-061-736

Query Match 2.0%; Score 43.6; DB 12; Length 1705;  
 Best Local Similarity 63.2%; Pred. No. 3.3;  
 Matches 67; Conservative 0; Mismatches 39; Indels 0; Gaps 0;  
 Qy 1027 AAATTTAGCTTAGCGTTTGAATTCGAATGAGGAAGATTATGTAACCTGAAAAATTTCTC 1086  
 Db 776 AAATTTATCTTTCTTTTGAATACTCAATTCACAAAGATTACATCACCGAAAGCTCTAC 835  
 Qy 1087 CAATCCCTGTTGCTGGAAGTCCCTGTGGTGTGTTGGTGCTCCAA 1132  
 Db 836 AATGCATTTTGGCTGCTCAGTACCTGTTGTTCTGGGACCATCCA 881

RESULT 3

US-11-128-049-736  
 ; Sequence 736, Application US/11128049  
 ; Publication No. US20060010513A1  
 ; GENERAL INFORMATION:

; APPLICANT: Melville, Mark W.  
 ; APPLICANT: Charlebois, Timothy S.  
 ; APPLICANT: Mounts, William M.  
 ; APPLICANT: Hann, Louane E.  
 ; APPLICANT: Sinacore, Martin S.  
 ; APPLICANT: Leonard, Mark W.  
 ; APPLICANT: Brown, Eugene L.  
 ; APPLICANT: Miller, Christopher P.  
 ; TITLE OF INVENTION: OLIGONUCLEOTIDE ARRAYS TO MONITOR GENE EXPRESSION AND METHODS FOR  
 ; TITLE OF INVENTION: MAKING AND USING SAME  
 ; FILE REFERENCE: 01997.027700  
 ; CURRENT APPLICATION NUMBER: US/11/128,049  
 ; CURRENT FILING DATE: 2005-05-11  
 ; PRIOR APPLICATION NUMBER: US 60/570,425  
 ; PRIOR FILING DATE: 2004-05-11  
 ; NUMBER OF SEQ ID NOS: 7285  
 ; SOFTWARE: PatentIn version 3.3  
 ; SEQ ID NO 736  
 ; LENGTH: 1705  
 ; TYPE: DNA  
 ; ORGANISM: Cricetulus griseus  
 ; FEATURE:  
 ; NAME/KEY: misc\_feature  
 ; LOCATION: (1505)..(1521)  
 ; OTHER INFORMATION: n is a, c, g, or t  
 US-11-128-049-736  
 Query Match 2.0%; Score 43.6; DB 12; Length 1705;  
 Best Local Similarity 63.2%; Pred. No. 3.3;  
 Matches 67; Conservative 0; Mismatches 39; Indels 0; Gaps 0;  
 Qy 1027 AAATTTAGCTTAGCGTTTGAATTCGAATGAGGAAGATTATGTAACCTGAAAAATTTCTC 1086  
 Db 776 AAATTTATCTTTCTTTTGAATACTCAATTCACAAAGATTACATCACCGAAAGCTCTAC 835  
 Qy 1087 CAATCCCTGTTGCTGGAAGTCCCTGTGGTGTGTTGGTGCTCCAA 1132  
 Db 836 AATGCATTTTGGCTGCTCAGTACCTGTTGTTCTGGGACCATCCA 881  
 RESULT 4  
 US-09-925-065A-65761  
 ; Sequence 65761, Application US/09925065A  
 ; Publication No. US20040181048A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wang, David G.  
 ; TITLE OF INVENTION: Identification and Mapping of Single  
 ; FILE REFERENCE: 108827.135  
 ; CURRENT APPLICATION NUMBER: US/09/925,065A  
 ; CURRENT FILING DATE: 2001-08-08  
 ; PRIOR APPLICATION NUMBER: US 60/243,096  
 ; PRIOR FILING DATE: 2000-10-24  
 ; PRIOR APPLICATION NUMBER: US 60/252,147  
 ; PRIOR FILING DATE: 2000-11-20  
 ; PRIOR APPLICATION NUMBER: US 60/250,092  
 ; PRIOR FILING DATE: 2000-11-30  
 ; PRIOR APPLICATION NUMBER: US 60/261,766  
 ; PRIOR FILING DATE: 2001-01-16  
 ; PRIOR APPLICATION NUMBER: US 60/289,846  
 ; PRIOR FILING DATE: 2001-05-09  
 ; NUMBER OF SEQ ID NOS: 957086  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 65761  
 ; LENGTH: 1141  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; ORGANISM: Homo sapiens  
 US-09-925-065A-65761  
 Query Match 1.9%; Score 41.6; DB 6; Length 1141;  
 Best Local Similarity 53.8%; Pred. No. 8.3;  
 Matches 86; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

QY 1531 TTGAAGTTCCATCCCTGAAATCTTGTGCTGTATGGAAGACTGAAAGGCTGAAAGTTATA 1590  
 DB 920 TTGAAGAACACCCGACTGTATCTCATGCTCGGGCTGACCAATGAGTAAGCAAAAGTGTTA 979  
 QY 1591 AGAGGGGGAGTGCTTTAAACTCTACAAAATATACCAATTTGGCTTGACACAGAGACAA 1650  
 DB 980 TCGGGGGAGACAGCCCTTCTAATTTCTGCAGACATTATTAATAATATCCAAACAGAGTACC 1039  
 QY 1651 GCTCTTTATACCTTCAGCTTCAAAGGTGATGCTGATTTCA 1690  
 DB 1040 GTGCAATCAATTTTCAGTTTCTAGGATGAGAGATATGTCA 1079

RESULT 5

US-11-112-908-297  
 ; Sequence 297, Application US/11112908  
 ; Publication No. US20050260659A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Harris, Cole  
 ; APPLICANT: Davis, Lisa M.  
 ; TITLE OF INVENTION: Breast Cancer Biomarkers  
 ; FILE REFERENCE: 04-164-US  
 ; CURRENT APPLICATION NUMBER: US/11/112,908  
 ; PRIOR FILING DATE: 2005-04-22  
 ; PRIOR APPLICATION NUMBER: US 60/564,758  
 ; PRIOR FILING DATE: 2004-04-23  
 ; PRIOR APPLICATION NUMBER: US 60/575,978  
 ; PRIOR FILING DATE: 2004-06-01  
 ; PRIOR APPLICATION NUMBER: US 60/631,702  
 ; PRIOR FILING DATE: 2004-11-30  
 ; PRIOR APPLICATION NUMBER: US 60/633,826  
 ; PRIOR FILING DATE: 2004-12-07  
 ; NUMBER OF SEQ ID NOS: 511  
 ; SOFTWARE: PatentIn version 3.3  
 ; SEQ ID NO 297  
 ; LENGTH: 1657  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-11-112-908-297

Query Match 1.9%; Score 41.6; DB 12; Length 1657;  
 Best Local Similarity 53.8%; Pred. No. 9.7;  
 Matches 86; Conservative 0; Mismatches 74; Indels 0; Gaps 0;  
 QY 1531 TTGAAGTTCCATCCCTGAAATCTTGTGCTGTATGGAAGACTGAAAGGCTGAAAGTTATA 1590  
 DB 1257 TTGAAGAACACCCGACTGTATCTCATGCTCGGGCTGACCAATGAGTAAGCAAAAGTGTTA 1316  
 QY 1591 AGAGGGGGAGTGCTTTAAACTCTACAAAATATACCAATTTGGCTTGACACAGAGACAA 1650  
 DB 1317 TCGGGGGAGACAGCCCTTCTAATTTCTGCAGACATTATTAATAATATCCAAACAGAGTACC 1376  
 QY 1651 GCTCTTTATACCTTCAGCTTCAAAGGTGATGCTGATTTCA 1690  
 DB 1377 GTGCAATCAATTTTCAGTTTCTAGGATGAGAGATATGTCA 1416

RESULT# 6

US-11-112-908-64  
 ; Sequence 64, Application US/11112908  
 ; Publication No. US20050260659A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Harris, Cole  
 ; APPLICANT: Davis, Lisa M.  
 ; TITLE OF INVENTION: Breast Cancer Biomarkers  
 ; FILE REFERENCE: 04-164-US  
 ; CURRENT APPLICATION NUMBER: US/11/112,908  
 ; PRIOR FILING DATE: 2005-04-22  
 ; PRIOR APPLICATION NUMBER: US 60/564,758  
 ; PRIOR FILING DATE: 2004-04-23  
 ; PRIOR APPLICATION NUMBER: US 60/575,978  
 ; PRIOR FILING DATE: 2004-06-01  
 ; PRIOR APPLICATION NUMBER: US 60/631,702

; PRIOR FILING DATE: 2004-11-30  
 ; PRIOR APPLICATION NUMBER: US 60/633,826  
 ; PRIOR FILING DATE: 2004-12-07  
 ; NUMBER OF SEQ ID NOS: 511  
 ; SOFTWARE: PatentIn version 3.3  
 ; SEQ ID NO 64  
 ; LENGTH: 157230  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-11-112-908-64

Query Match 1.9%; Score 41.6; DB 12; Length 157230;  
 Best Local Similarity 53.8%; Pred. No. 67;  
 Matches 86; Conservative 0; Mismatches 74; Indels 0; Gaps 0;  
 QY 1531 TTGAAGTTCCATCCCTGAAATCTTGTGCTGTATGGAAGACTGAAAGGCTGAAAGTTATA 1590  
 DB 106717 TTGAAGAACACCCGACTGTATCTCATGCTCGGGCTGACCAATGAGTAAGCAAAAGTGTTA 106776  
 QY 1591 AGAGGGGGAGTGCTTTAAACTCTACAAAATATACCAATTTGGCTTGACACAGAGACAA 1650  
 DB 106777 TCGGGGGAGACAGCCCTTCTAATTTCTGCAGACATTATTAATAATATCCAAACAGAGTACC 106836  
 QY 1651 GCTCTTTATACCTTCAGCTTCAAAGGTGATGCTGATTTCA 1690  
 DB 106837 GTGCAATCAATTTTCAGTTTCTAGGATGAGAGATATGTCA 106876

RESULT 7

US-11-112-908-62  
 ; Sequence 62, Application US/11112908  
 ; Publication No. US20050260659A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Harris, Cole  
 ; APPLICANT: Davis, Lisa M.  
 ; TITLE OF INVENTION: Breast Cancer Biomarkers  
 ; FILE REFERENCE: 04-164-US  
 ; CURRENT APPLICATION NUMBER: US/11/112,908  
 ; PRIOR FILING DATE: 2005-04-22  
 ; PRIOR APPLICATION NUMBER: US 60/564,758  
 ; PRIOR FILING DATE: 2004-04-23  
 ; PRIOR APPLICATION NUMBER: US 60/575,978  
 ; PRIOR FILING DATE: 2004-06-01  
 ; PRIOR APPLICATION NUMBER: US 60/631,702  
 ; PRIOR FILING DATE: 2004-11-30  
 ; PRIOR APPLICATION NUMBER: US 60/633,826  
 ; PRIOR FILING DATE: 2004-12-07  
 ; NUMBER OF SEQ ID NOS: 511  
 ; SOFTWARE: PatentIn version 3.3  
 ; SEQ ID NO 62  
 ; LENGTH: 170508  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-11-112-908-62

Query Match 1.9%; Score 41.6; DB 12; Length 170508;  
 Best Local Similarity 53.8%; Pred. No. 69;  
 Matches 86; Conservative 0; Mismatches 74; Indels 0; Gaps 0;  
 QY 1531 TTGAAGTTCCATCCCTGAAATCTTGTGCTGTATGGAAGACTGAAAGGCTGAAAGTTATA 1590  
 DB 90473 TTGAAGAACACCCGACTGTATCTCATGCTCGGGCTGACCAATGAGTAAGCAAAAGTGTTA 90532  
 QY 1591 AGAGGGGGAGTGCTTTAAACTCTACAAAATATACCAATTTGGCTTGACACAGAGACAA 1650  
 DB 90533 TCGGGGGAGACAGCCCTTCTAATTTCTGCAGACATTATTAATAATATCCAAACAGAGTACC 90592  
 QY 1651 GCTCTTTATACCTTCAGCTTCAAAGGTGATGCTGATTTCA 1690  
 DB 90593 GTGCAATCAATTTTCAGTTTCTAGGATGAGAGATATGTCA 90632

RESULT 8

US-11-112-908-65  
; Sequence 65, Application US/11112908  
; Publication No. US20050260659A1  
; GENERAL INFORMATION:  
; APPLICANT: Harris, Cole  
; APPLICANT: Davis, Lisa M.  
; TITLE OF INVENTION: Breast Cancer Biomarkers  
; FILE REFERENCE: 04-164-US  
; CURRENT APPLICATION NUMBER: US/11/112,908  
; CURRENT FILING DATE: 2005-04-22  
; PRIOR APPLICATION NUMBER: US 60/564,758  
; PRIOR FILING DATE: 2004-04-23  
; PRIOR APPLICATION NUMBER: US 60/575,978  
; PRIOR FILING DATE: 2004-06-01  
; PRIOR APPLICATION NUMBER: US 60/631,702  
; PRIOR FILING DATE: 2004-11-30  
; PRIOR APPLICATION NUMBER: US 60/633,826  
; PRIOR FILING DATE: 2004-12-07  
; NUMBER OF SEQ ID NOS: 511  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 65  
; LENGTH: 173115  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-112-908-65

Query Match 1.9%; Score 41.6; DB 12; Length 173115;  
Best Local Similarity 53.8%; Pred. No. 69;  
Matches 86; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

QY 1531 TTGAAGTTCCATCCCTCGAATCTTGCGCTGATGGAAGACTGAAAGCCCTGAAGTTATA 1590  
Db 42228 TTGAAGAACCAACCGACTGTATCTCATGCTCGGGCTGACCAATGAGTAAGCAAAAAGTGTTA 42287

QY 1591 AGAGGGGGAGTGCTTTAAAACCTCTACAAAATATACCAAAATGGCTTGACACAGACAA 1650  
Db 42288 TGGCGGGGACAGACGCTTCTAAATCTGCGACATTATTAAAATAATCCAAACACAGGTACCC 42347

QY 1651 GCTCTTTATACCTTCAGCTTCAAGAGTGATGCTGATTTCA 1690  
Db 42348 GTGCAATCAATTTTCAGTTCTTAGGATGAGAGATATGTCA 42387

RESULT 9  
US-09-925-065A-601955/c  
; Sequence 601955, Application US/09925065A  
; Publication No. US20040181048A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome  
; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US/09/925,065A  
; CURRENT FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: US 60/243,096  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/252,147  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: US 60/250,092  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: US 60/261,766  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/289,846  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 601955  
; LENGTH: 577  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-601955

Query Match 1.9%; Score 41.4; DB 6; Length 577;  
Best Local Similarity 62.4%; Pred. No. 6.9;  
Matches 63; Conservative 1; Mismatches 37; Indels 0; Gaps 0;

QY 10 AACGCTGCATTTCTTTTCTTTTCAGGGAACCATCCACCATAACCAACAAAAACAA 69  
Db 328 ATCATTCGAGCTTGCTGTTTTTGTAGTGATGACAAACAATAACCAACAAAAA 269

QY 70 CAGCAAGCTGTGTTTTTTTATCCTTTCTTTTAAACA 110  
Db 268 CAGGCTTTTCTGTTCCCTCATATGTTATTTTCTTTCAAAA 228

RESULT 10  
US-09-925-065A-486277/c  
; Sequence 486277, Application US/09925065A  
; Publication No. US20040181048A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US/09/925,065A  
; CURRENT FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: US 60/243,096  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/252,147  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: US 60/261,766  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/289,846  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 486277  
; LENGTH: 645  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-486277

Query Match 1.9%; Score 41; DB 6; Length 645;  
Best Local Similarity 62.6%; Pred. No. 9.1;  
Matches 62; Conservative 1; Mismatches 36; Indels 0; Gaps 0;

QY 564 AGAGCTATTTTGTCTCGAGCTGATCAGGAGTGAAGTCGTGTTGGTGTGATGTA 623  
Db 217 AGGGCTCCTTAATGTTTTCTGAGCTGTTCTCTTGCAATTGTTGAGTTTATATA 158

QY 624 ATTTCGGTTTAGTGGGATAGAAAGCCAGATGCCGCAAT 662  
Db 157 GATTAGGATTTCTGTCATTCGAGGGAAATGCTGNAAT 119

RESULT 11  
US-09-925-065A-566981  
; Sequence 566981, Application US/09925065A  
; Publication No. US20040181048A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US/09/925,065A  
; CURRENT FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: US 60/243,096  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/252,147  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: US 60/250,092  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: US 60/261,766  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/289,846  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 601955  
; LENGTH: 577  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-601955





Best Local Similarity 45.2%; Pred. No. 16;  
Matches 183; Conservative 1; Mismatches 218; Indels 3; Gaps 1;  
QY 1719 CAAGTTTGAAGTCATTTTGTGTAGCATGCGCTAAATGGTACCTCTGCTCTACCTGAATTT 1778  
Db 21 CAGGTTTGAACACACTCTTTTGTAGAAACTGCAAGGGGATAATTGCACTCTTTTGAGGAGT 80  
QY 1779 AGCTTCACCTAGCTGAGCAGTGTAGTATTTTAGGAATGAGTATGCGAGTGAATATGGC 1838  
Db 81 ACCGTAGTAAAGGAATAACTTCCTATARAAGACAGAGAGCTTTCTCAGAAAATCTCT 140  
QY 1839 ATGGCTTTTATTTATGCTAGTTTCTTGGCAACTCATTTGATGTTTGTATAAGACATCAC 1898  
Db 141 TTGGGATGATTGAGTTGAACCTCACAGAGCTGAGCAATTCCTTGGATGTAGCAGTTTAGAA 200  
QY 1899 AC---TTTAATTTTAAACTTTTCTGTAGAAAGTGCATAATCCATATTTAATGCTTAGTTT 1955  
Db 201 ACACACTTTCTGCAGAAATCTGCAAGTGCATATTTGGACCTCTGTGAGGAATTCGTTGAA 260  
QY 1956 TAGTGTCTTATCTGATCATCTAGAAGTCAAGTCTCTGTATATTTGTGAGTGAATACTGA 2015  
Db 261 ACGGGATAATTTTCTGAGCTGACTAAACAGAGAGTCTCAGAAATCTTCTTTGTGATGTTGC 320  
QY 2016 AATCTAATGAAGGATCAGATGTTTCTCACTCAAGACACATTTATTTATCTTCTGTTTGA 2075  
Db 321 ATTCAATATCCCGAGTTGAATTTCTTTCAGAGTTTCAAGTTTCAAGTTTCAAGTTTCA 380  
QY 2076 TGATCTCGAGCTTTTGTAGTGTCTGGAATCTGCTCCCTGTGGTTGA 2120  
Db 381 GGATCTACAAGTGGATATTTTGGACCACTCTGTGTCTTCTGTTTGA 425

Search completed: February 19, 2006, 18:25:01  
Job time : 653 secs

Query Match 1.8%; Score 40; DB 6; Length 600;  
Best Local Similarity 53.0%; Pred. No. 15;  
Matches 107; Conservative 1; Mismatches 91; Indels 3; Gaps 1;  
QY 1941 TTTAATGCTTAGTTTGTAGTGTCTTATCTGATCATCTAGAAGTCAAGTCTTCTGTATATT 2000  
Db 85 TTTTGTGACATTTTATGTTTGTGTTTGTAGTTTGTAGTTTGTAGTTTGTAGTTTGTAGTTT 144  
QY 2001 GTGAGTGAATACTGAATCTAATAGAAGGATCAGATGTTTCACTCAAGACACATTTATAC 2060  
Db 145 CTTAGGAAACAAAGTCTTTTATTATATGATAA---TTTCTGTGATTTGCTTTCTACT 201  
QY 2061 TTCAATGTTTGTGATGATCTCGAGCTTTTGTAGTGTGAACTGCTGCTGCTGTTGA 2120  
Db 202 TTCTGTGATGTTTACCAAGACACAAATTTTAAATTTTGTAGTGTCTAATTAATCTATTT 261  
QY 2121 GCACCTGTTATTGCTTCAAGTGT 2142  
Db 262 TCWTTTGTGTTGTGCTTTT 283

RESULT 15  
US-09-925-065A-325832  
; Sequence 325832, Application US/09925065A  
; Publication No. US20040181048A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome  
; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US/09/925,065A  
; CURRENT FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: US 60/243,096  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/252,147  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: US 60/250,092  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: US 60/261,766  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/289,846  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 325832  
; LENGTH: 504  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-325832  
Query Match 1.8%; Score 39.8; DB 6; Length 504;

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 19, 2006, 15:41:43 ; Search time 8807 Seconds  
(without alignment)  
11676.849 Million cell updates/sec

Title: US-09-913-858c-1

Perfect score: 2198

Sequence: 1 actaactcaaacgtcatt.....aaaaaaaaaaaaaaaaaaaaa 2198

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST:\*

1: gb\_est1:\*

2: gb\_est2:\*

3: gb\_est3:\*

4: gb\_hcc:\*

5: gb\_est4:\*

6: gb\_est5:\*

7: gb\_est6:\*

8: gb\_est7:\*

9: gb\_gss1:\*

10: gb\_gss2:\*

11: gb\_gss3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
c 1	533	24.2	861	8	CX710861 gmrtDrNS0
2	512.6	23.3	806	7	CO076716 GR_Ea38C
3	489.6	22.3	584	7	CV537942 NOD_248 D
c 4	462	21.0	782	8	CX710693 gmrtDrNS0
5	457.6	20.8	800	7	CX120486 218109.p1
6	447.6	20.4	863	6	CB669685 OSJNE02F
7	437.6	19.9	532	3	BM143091 saj39d07
8	430.4	19.6	862	8	DN798206 USDA-FP/A
c 9	422.8	19.2	865	6	CB656872 OSJNEC11L
10	414.4	18.9	744	6	CD813251 BN15_019A
11	401.4	18.3	818	7	CO072619 GR_Ea310
12	394.8	18.0	665	6	CD813104 BN15_001I
13	378.6	17.2	689	3	BM099511 EBes01_SQ
14	375.4	17.1	641	6	CF770670 DSBF1_9 C
15	371	16.9	599	7	CV534954 NOD_210 G
16	369.6	16.8	651	5	BQ592743
c 17	364.4	16.6	422	6	CA800844 sat25f03
18	354.2	16.1	539	1	AU292612 AU292612
19	341	15.5	551	3	CA008944 HU12K09r
20	337.2	15.3	571	3	BJ464838 BJ464838
21	332.2	15.1	517	2	BG790911 sae71e02
22	331.8	15.1	588	6	CF303361 ABF1--02-

23	326.2	14.8	811	6	CB566871
c 24	326	14.8	675	8	DR930577
25	321.2	14.6	683	6	CA197183
26	320.4	14.6	651	7	CN190564
27	317	14.4	842	7	CN818044
28	313.2	14.2	753	6	CB646605
29	292.4	13.3	700	8	DN157236
c 30	288.4	13.1	685	8	DN187833
31	284	12.9	729	6	CF770757
c 32	280.2	12.7	690	5	BQ659171
33	277.8	12.6	559	6	CA276866
c 34	276	12.6	722	8	DR814720
35	271.2	12.3	560	7	CK066728
36	269.6	12.3	793	8	DR174909
37	268	12.2	598	7	CK008937
c 38	262	11.9	911	10	CG142421
c 39	257.8	11.7	701	3	BQ167130
40	257.6	11.7	786	8	DN908926
41	256	11.6	606	7	CK764534
c 42	255.4	11.6	679	7	CO072618
43	255	11.6	831	6	CF446084
44	254.2	11.6	395	6	CF349923
45	252.8	11.5	832	8	DR818536

#### ALIGNMENTS

RESULT 1  
CX710861/c  
LOCUS CX710861 861 bp mRNA linear EST 21-JAN-2005  
DEFINITION gmrtDrNS01 24-D M13R C08 060.s4 Water stressed 48h segment 2  
gmrtDrNS01-Glycine max cDNA 3', mRNA sequence.

ACCESSION CX710861  
VERSION CX710861.1 GI:58024120  
KEYWORDS EST.

SOURCE Glycine max (soybean)

ORGANISM Glycine max

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;  
Glycine.

REFERENCE 1 (bases 1 to 861)

AUTHORS Valliyodan,B., Huang,S., Joshi,T., Hernandez,A., Spollen,W.G.,  
Bohnert,H.J., Duke,M.V., Liu,X., Scheffler,B.E., Sharp,R.E., Xu,D.,  
Springer,G.K., Stacey,G. and Nguyen,H.T.

TITLE EST Analysis of Soybean Root Tip Under Drought Stress: MSNC Grant  
02245 - Development and Deployment of Biotechnology Tools for  
Soybean Improvement

JOURNAL Unpublished (2005)

COMMENT Contact: Henry T. Nguyen

Molecular Genetics and Biotechnology  
University of Missouri-Columbia  
National Center for Soybean Biotechnology, 1-87 Agriculture Bldg.,  
MO 65211, USA  
Tel: (573)882-5494  
Fax: (573)882-1469  
Email: nguyenhenry@missouri.edu  
POLYA=Yes.

FEATURES

Location/Qualifiers  
1..861  
/organism="Glycine max"  
/mol\_type="mRNA"  
/cultivar="Williams82"  
/db\_xref="taxon:3847"  
/dev\_stage="Droughted Roots"  
/clone\_lib="gmrtDrNS01"  
/note="Vector: pBS II SK(+); Funding: The production of  
EST's submitted in this project was funded by MSNC Grant  
00245- Development and deployment of biotechnology tools  
for soybean improvement, to H.T. Nguyen as Principal  
Investigator. Sample collection and library construction:  
Dark grown soybean seedlings with primary roots were

transplanted to high (-0.05MPa) or low water potential (-1.6MPa) vermiculite, and harvested at 5h and 48h after transplanting. Each root tip was divided into two segments (distances are from the junction of root apex and root cap): segment 1, 0-3mm; and segment 2, 3-11mm. Total RNA was extracted by the 'hot phenol' method (Plant Molecular Biology manual, DS: 1-13, 2nd ed., 1997). This method worked in eliminating carbohydrate material present in the root tips. The integrity of the RNA was verified by denaturing agarose gels and spectrophotometry (ratio A260/280). Poly(A)<sup>+</sup>mRNA was isolated twice from total RNA using the Oligotex Direct mRNA kit (Qiagen). Poly(A)<sup>+</sup>mRNA was converted to double-stranded cDNA and tagged by using modified Oligo(dT) primers. The double stranded cDNAs were size-selected (>500 bp). Size selected cDNAs were adsorbed with EcoRI adaptors at both ends, and then digested with NotI. The cDNA was directionally cloned into the EcoRI-NotI digested pBS II SK(+) phagemid vector (Stratagene) and electroporated into E.coli DH10B. The gmrtDAGS01 library was created by subtracting the well-watered soybean root library from the water-stressed (5h and 48h) soybean root libraries. The double stranded plasmid DNA from the primary library was converted to single-stranded circles and used as a template for PCR amplification. The purified PCR products, representing the entire cDNA population cloned were used as a driver for normalization. Hybridization between the single-stranded library and the PCR products was carried out for 44 hours at 306C. Non-hybridized single-stranded DNA circles were separated from hybridized DNA rendered partially double-stranded and electroporated into DH10B E. coli. Clone requests: Requests for clones should be made to Dr. Henry Nguyen, National Center for Soybean Biotechnology, 1-87 Agriculture Bldg., University of Missouri-Columbia, MO, 65211. Email: [nguyenhenry@missouri.edu](mailto:nguyenhenry@missouri.edu)  
TAG TISSUE=water stressed 48h segment 2  
TAG\_SEQ=TCGGA"

## AUTHORS

Ramirez M., Graham M.A., Blanco-Lopez L., Silvente, S.,  
Medrano-Soto, A., Blair, M.W., Hernandez G., Vance, C.P. and Lara M.  
Sequencing and Analysis of Common Bean ESTs. Building a Foundation  
for Functional Genomics  
Plant Physiol. 137 (4), 1211-1227 (2005)

## JOURNAL

15824284

## PUBMED

Contact: Blanco-Lara, L.  
Nitrogen Fixation Centero  
National Autonomous University of Mexico  
Apartado Postal 565-A, Cuernavaca, Morelos, Mexico  
Tel: 52 777 3291815  
Email: blanco@cihn.unam.mx

## COMMENT

Seq primer: T3.  
Location/Qualifiers  
1..584  
/organism="Phaseolus vulgaris"  
/molecule="mRNA"  
/cultivar="Negro Jamaica 81"  
/db\_xref="taxon:3885"  
/dev stage="15 days post inoculation with Rhizobium  
tropici CIAT 899"  
/lab host="SOLR"

## FEATURES

source  
1..584  
/organism="Phaseolus vulgaris"  
/molecule="mRNA"  
/cultivar="Negro Jamaica 81"  
/db\_xref="taxon:3885"  
/dev stage="15 days post inoculation with Rhizobium  
tropici CIAT 899"  
/lab host="SOLR"

## ORIGIN

Query Match 22.3%; Score 489.6; DB 7; Length 584;  
Best Local Similarity 91.1%; Pred. No. 6.1e-118;  
Matches 532; Conservative 0; Mismatches 49; Indels 3; Gaps 1;

QY 649 CCAGATCCGATTTGGTTACCTCAACCAAGTGGACAGCTAGCATTCGCGATCAATG 708  
Db 1 CCTGATGCTGCTTTGGTTTCCCTC-CCAATCTGGAGTAGTAGTGCTCGCTCGATG 59  
QY 709 GAATCAGCAGAAATCTACTGCTGAGAACAAATATTCCTATGGCAAGCAGGAGGGATATAAC 768  
Db 60 GAATCCGCTTCTGTAATTCAGAGATAATCTTCCCAAGGCAACGAGGAGGGTTACGAT 119  
QY 769 ATCGTAATGACCAACAGCTCTATCTTCGGATGTTCTGTTGATATTTTTCATGGGCTGAG 828  
Db 120 ATTGTAATGACCAACAGCTCTATCTTCGGATGTTCTGTTGATATTTTTCATGGGCGGAG 179  
QY 829 TATGATATGATGGCAGCAGTCCAGCGGAAATCTGAAGCTCTCTTTCAGCTGCTTTCATT 888  
Db 180 TATGATATCATGGCAGCAGTCCAGCGGAAATCTGAAGCTCTCTTTCAGCTGCTTTCATT 239  
QY 889 TCCAAATTTGTTGCTCGAAATTTCCGGTTGCAAGCTCTTGAAGGCTTTGAAATCAAAAC 948  
Db 240 TCTAATTTGTTGCTCGGCACTTTCTGTTGGAAGCCTTTGTTGGCTTTGAAAGGCAAT 299  
QY 949 ATCAAAATTTGATTTATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1008  
Db 300 ATCAAGATAGATTTCTTATGTTAGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 359  
QY 1009 GAAGCCCTGAGCACTACAAATTTAGCTTAGCTTTGAAATTTGAAATTTGAAATTTGAAATTTG 1068  
Db 360 GAAATCTGAAACGCTTAAGTTTAGCTTTGAAATTTGAAATTTGAAATTTGAAATTTGAAATTTG 419  
QY 1069 GTAATGAAATTTCTTCAATCCCTGTTGCTGGAACCTGCTTCTGTTGTTGTTGTTGTTGTTG 1128  
Db 420 GTCATGAAATTTCTTCAATCCCTGTTGCTGGAACCTGCTTCTGTTGTTGTTGTTGTTGTTG 479  
QY 1129 CCNAATATTCAGACTTTGCT 1188  
Db 480 CCAAAATTTGAAGACTTTGCAACCGTCTCCAGTTTCATATTTACATATCAAGGAACTGGAG 539  
QY 1189 GATGTTGATGCTGTTGCAAGACATGAGATATCTAGCAGAAATCCGAGCATATATAT 1248  
Db 540 GATGTTTCCATCAATTTGCAAGAAATGAACTGCTCGAGAAATCCGAGCATATATAT 599  
QY 1249 CAATCATTGAGTGGAGTATGAGGTCCTCTGACTCTCTTCAAGGCTCTTGTGGATG 1308  
Db 600 CAATCACTAAGTGGAGTATGAGGTCCTCTGACTCTCTTCAAGGCTCTTGTGGATG 659  
QY 1309 GCAGCTGTCATTCATCTGCGCTTTTTCATTTCACTTTGCGCAAGTGGAGTGGAGAGAG 1368  
Db 660 GCTGCTGTTTCATTCATCATGTCGGTTGTGCATTCACITGGCAACCGTCTATCCAAAGAGAAA 719  
QY 1369 GAAGAAATATCCAAAGCTTAAGAGAGCTCTTCAAGTGCATTCAGAGGCTTGGAGGCTTGAAG 1428  
Db 720 GAAGAAAGAGCTCCGACTTCAAGAAACGCTCTGCAAGTGTACAGAGGTTTCAAGAAC 779  
QY 1429 GTATATCATATCTATGTCAGAGA 1451  
Db 780 GTGATCATATATGTAAGAGA 802

## RESULT 3

## CV537942

## LOCUS

## DEFINITION

## NOD\_248\_D02 Phaseolus vulgaris nodule EST library Phaseolus

## vulgaris cdna 5', mRNA sequence.

## CV537942

## ACCESSION

## CV537942.1 GI:62711346

## KEYWORDS

## EST

## SOURCE

## Phaseolus vulgaris

## ORGANISM

## Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

## Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

## rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;

## Phaseolus.

## REFERENCE

## 1 (bases 1 to 584)



RESULT 5	CK120486	800 bp	mRNA	linear	EST 01-JUN-2004
LOCUS	218i09.p1	AtM1 Arabidopsis thaliana	CDNA clone	MPMGp2011i09218	
DEFINITION	5-PRIME, mRNA sequence.				
ACCESSION	CK120486				
VERSION	CK120486.1	GI:47830802			
KEYWORDS	EST.				
SOURCE	Arabidopsis thaliana (thale cress)				
ORGANISM	Arabidopsis thaliana				
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.				
REFERENCE	1 (bases 1 to 800)				
AUTHORS	Feilner,T., Immlink,R.G.H., Cahill,D.J. and Kersten,B.				
TITLE	Generation of a cDNA expression library from Arabidopsis fluorescence meristem				
JOURNAL	Unpublished (2003)				
COMMENT	Contact: Birgit Kersten Plant Protein Chip Group, Department Lehrach Max-Planck-Institute for Molecular Genetics Ilnestr. 73, D-14195 Berlin, Germany Tel: +49(0)30/84131648 Fax: +49(0)30/84131128 Email: Kersten@molgen.mpg.de Insert Length: 800 Std Error: 0.00 Plate: 218 row: I column: 9 Seq primer: pOE65.				
FEATURES	Location/Qualifiers				
source	1..800				
	/organism="Arabidopsis thaliana"				
	/mol_type="mRNA"				
	/ecotype="Columbia"				
	/db_xref="GABI:955906"				
	/db_xref="taxon:3702"				
	/clones="MPMGp2011i09218"				
	/tissue_type="inflorescence meristem"				
	/dev_stage="about one week after bolting"				
	/lab_host="E. coli SCS-1/pSE111"				
	/clone_lib="AtM1"				
	/note="vector: pOE-30NAST-attB (AY386205); Site_1: SalI; Site_2: NotI; About 1 week after bolting, cDNA synthesis using SuperscriptTM-system (Invitrogen) with an oligo(dT)-primer containing NotI restriction site and a SalI adapter. The main library (plate numbers begin with 1) of 38,000 clones was rearrayed into the sublibrary (plate numbers begin with 201) containing 5,000 putative expression clones. Average insert size is 1 kb. Note: The rearrayed sublibrary (plate numbers begin with 201) was sequenced. Library generation and sequencing was granted in context of GABI-LAPP; data are also accessible at https://gabi.rzpd.de"				
ORIGIN					
Query Match	20.8%;	Score 457.6;	DB 7;	Length 800;	
Best Local Similarity	73.8%;	Pred. No. 2e-109;			
Matches 580;	Conservative 0;	Mismatches 206;	Indels 0;	Gaps 0;	
QY	633	TAGTGGGGATAGAAAGCCAGATGCCGATTTGGGTACCTCAACCAAGTGGAAACAGCTAG 692			
Db	5	TAGTTTCAGGGAAACACCCAGATGTCGGTTGGATTAGGTTCAGAAACCTGGAACTCTTAG 64			
QY	693	CATTCTCCGATCAATGCAATCAGCAGAACTACTATGCTGAGAACAAATATTCGCATGGCAAG 752			
Db	65	TATAATACGTTCCATGGAATCAGCACAGTATTATCCAGAAATGATCTTGACAGGCAGC 124			
QY	753	ACGAGAGGGGATATAACATCGTAATGACAAACCAAGTCTATCTTCGGATGTTCTCTGTTGGATA 812			
Db	125	ACGAGAGGTTATGATATAGTAGTGACCACTAGTCTATCATCAGATGTTCTCTGTTGGATA 184			
QY	813	TTTTTCATGGCGTAGTATGATATGATGGACACCAAGTGCAGCCGAAAAAATGAAGTCGTCT 872			
Db	185	TTTTTCCTGGCGGAGTATGATATTATGTTCTCCGGTACAGCAAAAATCTGAGAGAGCTAT 244			





```

Matches 473; Conservative 0; Mismatches 59; Indels 0; Gaps 0;
Qy 1209 GACCATGAGATATCTAGCAGAAATCCGAGCATATATAAATCAATCATTTGAGTGGAGTA 1268
Db 1 GTCCATGAGATACCTAGCAGAAATCAAGCAGCGTATATAATCAATCGTTGAGGTGGAAGTA 60
Qy 1269 TGAGGTCCATCTGACTCTTCAAGGCCCTTGTGGATATGCGAGCTGTGCATTCATCGTG 1328
Db 61 TGAGGCCCATCTGATTCCTTCAAGGCCCTTGTGGATATGCGAGCTGTACATCTTCTCTG 120
Qy 1329 CCGTCTTTGCAATTCATCTGGCCACAGTGTAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1388
Db 121 CCGCCTTTGCAATTCATCTGGCCACAGTGTAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
Qy 1389 TAAGAGAGCTCTTGCAGTGCATCTAGAGGCCAGAGAACCGTATATCATATCTATGTCAG 1448
Db 181 CAACAAAGCCCTTGCAGTGCATCTAGAGGCCAGAGAACCGTATATCATATCTATGTCAG 240
Qy 1449 AGAAGGGGAGAGTGTGAGATGGAGTCCATTTTACCTGAGGTCTAGCAATTTAACTCTGAA 1508
Db 241 AGAAGGGGAGAGTGTGAGATGGAGTCCATTTTACCTGAGGTCTAGCAATTTAACTCTGAA 300
Qy 1509 TGCTGTGAAGCTCTGTGTTTGAAGTTCACATCCCTGAATCTTGTGCTGTATGAGAA 1568
Db 301 GGCCTTGAAGTCTGAGTGTGTTTGAAGTTCACATCCCTGAATCATGTACCTATATGAA 360
Qy 1569 GACTGAAGGCTGAAGTATTAAGAGGGGGAGTGTCTTAAACTCTACAAATATATACCC 1628
Db 361 GACAGAAAGACCTGAAGTCTTGAAGGGGGAGTGTCTTAAACTCTACAAATATATACCC 420
Qy 1629 AATTGGCTTGACACAGAGACAGTCTTTATACCTTCAGCTTCAAGGTGTAGTGTGATTT 1688
Db 421 AGTTGGTTTGACACAGAGACAGTCTTTATACCTTCAGCTTCAAGGTGTAGTGTGATTT 480
Qy 1689 CAGGAGTCACTTGGAGACAACTCTTGTGCCAAGTTTGAAGTCAATTTTGTG 1740
Db 481 CAGGAGTCACTTGGAGACCACTCTTGTGCCAAGTTTGAAGTCAATTTTGTG 532

```

```

RESULT 8
DN798206 862 bp mRNA linear EST 08-APR-2005
LOCUS DN798206
DEFINITION USDA-FP/ARO 13074 Star Ruby grapefruit temperature-conditioned
flavado cDNA Citrus x paradisi cDNA clone Cond-32_C09 5', mRNA
sequence.
ACCESSION DN798206
VERSION DN798206.1 GI:62430012
KEYWORDS Citrus x paradisi
SOURCE Citrus x paradisi
ORGANISM Citrus x paradisi
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Sapindales; Rutaceae; Citrus.
1 (bases 1 to 862)
McCollum T.G., Maul, P. and Porat, R.
Expressed Sequence Tags (ESTs) from Flavado of Star Ruby grapefruit
after temperature conditioning
JOURNAL Unpublished (2005)
COMMENT Contact: McCollum, T.G.
US Horticultural Research Laboratory
USDA, ARS
2001 S. Rock Road, Ft. Pierce, FL 34945, USA
Tel: 561-462-5836
Fax: 561-462-5986
Email: gmcollum@ushrl.ars.usda.gov
Seq primer: T3 Primer.
FEATURES
source
Location/Qualifiers
1..862
/organism="Citrus x paradisi"
/mol_type="mRNA"
/db_xref="taxon:37656"
/clone="Cond-32_C09"
/tissue_type="flavado"

```

```

/dev stage="mature fruit"
/lab host="SOLR"
/clone lib="Star Ruby grapefruit temperature-conditioned
flavado cDNA"
/notes="Organ: fruit; Vector: pBluescript II SK-; Site_1:
EcORI; Site_2: XhoI; Standard library construction
protocols from Stratagene cDNA synthesis kit (Cat No.
20401-5) and Uni-ZAP XR vector kit (Cat No. 237211). A
high quality EST with at least 150 contiguous bases at
Trace Tuner score of 20 or better."

ORIGIN
Query Match 19.6%; Score 430.4; DB 8; Length 862;
Best Local Similarity 69.3%; Pred. No. 3.1e-102;
Matches 671; Conservative 0; Mismatches 191; Indels 106; Gaps 2;

Qy 729 TGAGAAACAATATTCCTGATGATATTTTTCATGGCTGAGTATGATATGATGACCAAGT 788
Db 1 TGAGAAACAATATTCCTGATGATATTTTTCATGGCTGAGTATGATATGATGACCAAGT 60
Qy 789 ATCTTCGATGTTTCTGATGATATTTTTCATGGCTGAGTATGATATGATGACCAAGT 848
Db 61 CTATCATGATGTTTCTGATGATATTTTTCATGGCTGAGTATGATATGATGACCAAGT 120
Qy 849 GCAGCCGAAACCTGAGCTGCTTTGAGCTGCTTTTCAATTTCCAAATGTTGTTGCTCGAAA 908
Db 121 GCAGCCGAAACCTGAGCTGCTTTGAGCTGCTTTTCAATTTCCAAATGTTGTTGCTCGAAA 180
Qy 909 TTTCCGGTGGAGCTCTTGAAGCCCTTGAAGAAATCAAAATCAAAATGATTTGTTATG 968
Db 181 CTTCCGGTGGAGCTCTTGAAGCCCTTGAAGAAATGTAAGATAGATATCATATG 240
Qy 969 TGGTTGTCAGAGAACCTGATGAGAGTGAACAAAGTGAAGCCCTGAAGCACTACAA 1028
Db 241 TGGTTGCCACCGAATCGTATGGAAGA----- 268
Qy 1029 ATTTAGCTTAGCGTTTGAATAATTCGAATGAGAGAGATATGTAATGAAAAATTTCTTCCA 1088
Db 269 ----- 268
Qy 1089 ATCCCTTGTGCTGGAACCTGCTGCTGTTGTTGTTGCTCCAAATATTCAGAGCTTTGC 1148
Db 269 -----GGATCGGTCCCTGCTGTTGTTGTTGCTCCAAATATTCAGAGATTTTGC 315
Qy 1149 TCCTTCTCCTGTTCAATTTTACATATTTAAAGAGATAGAGATGTTGATGCTGTTGCAAA 1208
Db 316 TCCTTCTCCTGAGTCAATTTTACATATTCGAGAGAGAGAGATGTTCAAGTCTGTTGCCAA 375
Qy 1209 GACCATGAGATATCTAGCAGAAAAATCCGAGACATATAATCAATCATTTGAGGTGGAAGTA 1268
Db 376 GACCATGAAATACCTTGCAGAAAAATCCTGAGGCATATAATCAGTCACCTAAGTTGGAAGTA 435
Qy 1269 TGAGGTGTCATCTGACTCTCTTCAAGGCCCTTGTGGATATGCGAGCTGTGCATTCATCGTG 1328
Db 436 TGAAGGGCCCTCTGATTTCTTCAAGGCACCTTGTGGATATGCTGCGAGTACATCATCATG 495
Qy 1329 CCGTCTTTGCAATTCATCTGGCCACAGTGTAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1388
Db 496 TCGTCTTTGATTTTACCTGGCAACAAAGATTTCAGAGAGAGAGAGAGAGAGAGAGAGAG 555
Qy 1389 TAAGAGAGCTCTTTCAGAGTGCATCTAGAGGCCAGAGAACCGTATATCATATCTATGTCAG 1448
Db 556 CAGGAAAGCCCTTGCAGAGTGCACAGAGGTTTCGGAACCTGTGCATCATTTGTATGTCAG 615
Qy 1449 AGAAGGGGAGAGTGTGAGATGAGTGCATTTTACCTGAGGTCTAGCAATTTAACTCTGAA 1508
Db 616 GGAAGAGAGGAGGTTTCAAAATGGTATCCATTTTCTTAAAGGTCTGCGAGTTTGACACTAAA 675
Qy 1509 TGCTGTGAGAGCTCTGTTGTTTGAAGTTCACATCCCTGAATCTTGTGCTGTATGAA 1568
Db 676 GGCCTTGGAAATCTTCAGTGTGGCAAGTTCAGTCTCTAAAACACAGTGCCTAATTTGAA 735
Qy 1569 GACTGAAAGGCTCTGAAGTTATATAAGAGGGGGAGTGTCTTTAAACTCTCTAATAATATACCC 1628

```









181 ACCGTGATGGCAAGTGGGCAAAAGTGGACACTTTGAAACGCTACAGATTCAGCTTGGCAT 240  
1043 TTGAAAATTCGAATGAGGAGATATGTAACTGAAAAATTCCTCCAAATCCCTTGTGTG 1102  
241 TTGAGAAATTCATAGAGGAGATACGTAACAGAAAAGTTTTCAGTCACTGGTAGCAG 300  
1103 GAATCTGCTGCTGGTGTGGTGGTCCAAATATTCAGGACTTGTCTCTCTCTGGTT 1162  
301 GTTCTATTCAGTTGTTGTGTGCTCCAAATATTCAGAGATTTTCTCCGGGAGAGGTG 360  
1163 CAATTTTACATATAAGAGATAGAGGATGTCAGTCTGTGCAAAAGACATGAGATATC 1222  
361 CAATATTTACATATAAGGAACTTGTGATGTCCTTCAGTTGCTTAAGACAATGAAAAATA 420  
1223 TAGCAGAAAATCCCGAAGCATATAATCAATCAATTCAGGTGGAGTATGAGGTCCATCTG 1282  
421 TTGCTCAATCTGATGCTTCAATCAATCTTTGAGGTGGAGTATGATGTCCTCTG 480  
1283 ACTCTTCAAGCCCTTGTGGATATGCGAGCTGTGCAATTCATCGTCCGCTCTTTGCATTC 1342  
481 ATTCTTCAAGCCCTTATGACATGCGACGAGTTCATTCATCTTGTGCTCTTTGTATAC 540  
1343 ACTTGGCCAGCTGAGTAGAGAGAGAGAAATATCAAGCCTTAAGAGACGTCCTT 1402  
541 ATATTGCTACCAAGATCCAGTTAAAGAGAGAAATGACTCCAAATTTTACAAATCGTCCTT 600  
1403 GCAAGTGCCTAGAGGCCAGAAACCGTATATATCATATCTAT 1443  
601 GTAGCTGTTCCAGCAAAAAGGAAACAGTTTACCACATATT 641

RESULT 15  
CV534954  
LOCUS  
DEFINITION  
NOD\_210\_G07 Phaseolus vulgaris nodule EST library Phaseolus  
vulgaris cDNA 5', mRNA sequence.

CV534954  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Phaseolus vulgaris  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;  
Phaseolus.  
1 (bases 1 to 599)  
Ramirez,M., Graham,M.A., Blanco-Lopez,L., Silvente,S.,  
Medrano-Soto,A., Blair,M.W., Hernandez,G., Vance,C.P. and Lara,M.  
Sequencing and Analysis of Common Bean ESTs. Building a Foundation  
for Functional Genomics  
Plant Physiol. 137 (4), 1211-1227 (2005)  
15824284  
Contact: Blanco-Lara, L.  
Nitrogen Fixation Centro  
National Autonomous University of Mexico  
Apartado Postal 565-A, Cuernavaca, Morelos, Mexico  
Tel: 52 777 3291815  
Email: blanco@cifn.unam.mx

Seq primer: T3.  
FEATURES  
source  
1. .599  
/organism="Phaseolus vulgaris"  
/mol\_type="mRNA"  
/cultivar="Negro Jamaica 81"  
/db\_xref="taxon:3885"  
/dev\_stage="15 days post inoculation with Rhizobium  
tropici CIAT 899"  
/lab\_host="SOLR"  
/clone\_lib="Phaseolus vulgaris nodule EST library"  
/note="Organ: Nodules; Vector: pBluescript SK(+); Site\_1:  
EcoRI; Site\_2: XhoI; Total RNA was prepared from P.  
vulgaris nodules, 15 days post inoculation with Rhizobium  
tropici CIAT 899. Poly (A+) RNA was obtained from total

RNA using oligo (dT) cellulose. Poly (A+) RNA was reverse  
transcribed and cloned in the Uni-Zap XR vector  
(Stratagene). Plasmids containing cDNAs were then excised  
from the Uni- Zap XR vector and propagated in SOLR cells.  
All sequences were searched for vector segments to check  
for insert integrity. The sequences contain a minimum of  
90 high quality bases and have been trimmed to remove  
vector and adaptor sequences."

ORIGIN

Query Match 16.9%; Score 371; DB 7; Length 599;  
Best Local Similarity 85.9%; Pred. No. 1.5e-86;  
Matches 437; Conservative 0; Mismatches 65; Indels 7; Gaps 2;  
QY 2 CTAACTCAAAACGCTGCAATTTCTTTTCTTTCAGGGAACCATCCACCATAACACAAA 61  
DB 91 CTAACTCAAAACGCTGCAATTTTCTCTTTTGGGAACCATCCACCATAAAGACAAC 150  
QY 62 AAAAAACACAGC---AAGCTGCTTTTATCGTTCTTTTCTTTTAAACAAAGCACCC 117  
DB 151 AAAAAACACAGCAGTAAAGCTGTGTTTTTGTGTCATTTTTTCTTTTAAACAGCACCC 210  
QY 118 CCATCATGGAATCGTCTCATAAACGCAAAATTTTCCATTTCCCTTTGATTTTATGTTA 177  
DB 211 CCATCATGGAATCCTGCCCATTAACGCAATATTCCGTTTCCCTTTTCAATTTTGTTC 270  
QY 178 TTTTGGGAATTTGGCAGTTTGGGGGCGCAATTGAATGATGGGTCTGTTGACGATCTTCGA 237  
DB 271 TTTTGGGAATTTGGGAGTTGGAGGCGCAATCGAATGATGGGTCTGGTCAAGATCTTCGA 330  
QY 238 GGCTCGAGAACAGATGGTCCCAACAAAGACAGCTTACCCGTTTGTGGCTCCGGGAGCAAC 297  
DB 331 GGTTCAAGAACAGAGGGTGCCCAACAAAGAGAGATGCCCGTTTGGCTCCGGGTGGCAAC 390  
QY 298 CCAAAGAGGAAATGGAGCAATCTAATGCCTCTTTGTTGTTGCCCTTGTGTGTCATCGGGAG 357  
DB 391 CCAAAGAGGAAATGGAGCAATCTAATGCCTCTTTGTTGTTGCCCTTGTGTGTCATCGGGAG 450  
QY 358 ATCGCGTTTCTGGGTAGGTGGATATGGCCAAACACCGCCCATGGTTGACTCCCTCGCT 417  
DB 451 ATCGCGTTTCTGGGTAGGTGGATATGGCCAAACACCGCCCATGGTTGACTCCCTCGCT 510  
QY 418 GACTTCTTCTACCGCTCTCGAGCGGTCTTGAAGGTGACGATTTGGGGTTGGGT---TTG 474  
DB 511 GACTTCTTCTACCGCTCTCTGTCGGTCTGTTGAAGGTGACGATTTGGGGATGGGTGGT 570  
QY 475 GTGGCTTCTGATCGGAATTTCTGAATCGTA 503  
DB 571 GTGGCTTCTGATCGGAATTTCTGAATCGGA 599

Search completed: February 19, 2006, 18:14:06  
Job time : 8812 secs